

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 08:24:20 ; Search time 160.586 Seconds
(without alignments)
3175.877 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	4892	96.3	3768	4	US-09-811-115-2
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8	4892	96.3	4530	1	US-08-645-865-9
9	4892	96.3	4530	1	US-09-167-322-4
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18	3471	68.4	1872	3	US-08-422-108-2	Sequence 2, Appl
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20	1645	32.4	5532	2	US-08-475-035-3	Sequence 3, Appl
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25	1435	28.3	4905	1	US-07-978-895-3	Sequence 3, Appl
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29	1435	28.3	4975	3	US-09-630-706-3	Sequence 3, Appl
30	1311	25.8	4545	6	5183884-3	Patent No. 5183884
31	1032	20.3	1958	4	US-09-570-454-1	Sequence 1, Appl
32	1032	20.3	1958	4	US-09-867-521-1	Sequence 1, Appl
33	942	18.6	1593	4	US-09-676-610B-25	Sequence 25, Appl
34	942	18.6	1868	1	US-08-658-883B-1	Sequence 1, Appl
35	942	18.6	1868	4	US-09-676-610B-26	Sequence 26, Appl
36	493	9.7	322	1	US-08-421-356-1	Sequence 1, Appl
37	493	9.7	322	4	US-09-046-783-1	Sequence 1, Appl
38	381	7.5	4149	2	US-08-737-715-1	Sequence 1, Appl
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40	376	7.4	2533	3	US-09-149-922-5	Sequence 5, Appl
41	335	6.6	4989	2	US-08-625-819-1	Sequence 1, Appl
42	335	6.6	4989	4	US-09-343-551-1	Sequence 1, Appl
43	333	6.6	4975	2	US-08-249-687C-1	Sequence 1, Appl
44	333	6.6	4989	2	US-08-666-392A-3	Sequence 3, Appl
45	333	6.6	4989	3	US-08-753-558-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3768 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3765
 US-08-625-101-1

Alignment Scores:

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 Score: 4900.00 Matches: 919
 Percent Similarity: 73.23% Conservatives: 0
 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
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US-09-493-480-6 (1-919) x US-08-625-101-1 (1-3768)

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 Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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 Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
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RESULT 2

US-08-356-786-1

; Sequence 1, Application US/08356786

; Patent No. 5877305

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; APPLICANT: Oppermann, Hermann

; APPLICANT: Houston, L. L.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault

; STREET: Exchange Place, 53 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,786
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/831,967
 FILING DATE: 06-FEB-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pitcher, Edmund R.
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: CRP-053
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3768 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3768
 OTHER INFORMATION: /note= "product = "cerB-b2"
 US-08-356-786-1

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 4900.00 Matches: 919
 Percent Similarity: 73.23% Conservative: 0
 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
 DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-08-356-786-1 (1-3768)

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601	G	G	C	T	C	C	G	C	T	G	G	G	A	G	A	G	T	660
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781	A	G	T	G	G	C	A	T	C	T	G	A	C	T	C	T	C	840
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1021	G	T	G	T	G	T	G	G	C	A	T	T	G	G	A	G	G	1080
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1081	A	T	C	A	G	A	G	T	T	C	T	T	T	G	G	A	G	1140
381	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Glu	Gln	Leu	Gln	Val	Phe	400
1141	T	T	T	G	A	T	G	G	A	C	T	T	T	T	T	T	T	1200
401	Glu	Thr	Leu	Glu	Glu	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	420
1201	G	A	C	T	C	T	G	A	G	A	T	C	A	T	C	T	C	1260
421	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	Gly	Arg	Ile	Leu	His	440
1261	G	A	C	T	C	A	G	A	C	T	T	C	C	A	G	A	T	1320
441	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	460
1321	T	A	C	T	C	G	T	G	A	G	G	C	T	G	G	C	T	1380
461	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	480
1381	C	T	G	G	C	A	T	C	C	A	T	A	C	C	C	C	C	1440
481	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	His	Thr	Ala	Asn	500
1441	C	C	T	G	G	A	C	C	A	G	C	T	C	T	G	C	A	1500
501	Glu	Asp	Glu	Cys	Val	Gly	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	520
1501	G	A	G	A	C	A	G	T	G	G	C	C	T	G	C	C	C	1560
521	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	540

1561 TGGGTCAGGGCCACCCAGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGAGTGC 1620
541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
1621 GTGGAGGAATGCCGAGTACTGCAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACCTGT 1680
561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
1681 TTGCGGTGCCACCTCTAGTGTGACGCCCCAGAAATGGCTCAGTGACCTGTTTGGACCGGAG 1740
581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
1741 GCTGACCAAGTGTGGCGCTGTGCCCACTATAGGACCTCTCCCTCTGGTGGCCCGCTGC 1800
601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
1801 CCCAGCGGTGTGAACCTGACCTCTCTTACATGCCCCATCTGGAGTTTCCAGATGAGGAG 1860
621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
1861 GGCCGATGCCAGCTTGGCCCATCAACTGCACTCCCACTCTGTGTGGACCTGTGATGACAA 1920
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
1921 GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGAGTCCATCATCTCTGCGGTGGTTGGC 1980
653 ----- 653
1981 ATTCTGTGGTGGTGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGAGCGGAGCAG 2040
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2041 AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAACCGAGCTGTGTGGAGCCGCTG 2100
653 ----- 653
2101 ACACCTAGCGGAGCGATGCCCAACAGCGGCGAGATGCGGATCTCTGAAGAGACGGAGCTG 2160
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2161 AGGAAGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAGGGGCATCTGGATC 2220
653 ----- 653
2221 CCTGATGGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAGTGTTCAGGGGAAACACATCC 2280
653 ----- 653
2281 CCCAAGCCAAAGAAATCTTAGACGAGCATACGTGATGGTGTGGGTCCCA 2340
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2341 TATGTCTCCCGCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGTGACACAGCTT 2400
653 ----- 653
2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCCGGAAGCTTGGGCTCCAG 2460
653 ----- 653
2461 GACCTGTGAATCTGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGGGG 2520
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2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
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2581 ATTACAGACTTGGGGTGGCTCGGCTGTGGCATTTGACGACATTTGACGACAGAGTACCATGCAGAT 2640
653 ----- 653

2641 GGGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTTCGCGCGGGTTCACC 2700
653 ----- 653
2701 CACCAGAGTGTGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
653 ----- 653
2761 AAACCTTAGATGGATCCAGCCCGGAGATCCCTGACCTCTGTGAAAGGGGAGCGG 2820
653 ----- 653
2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTCTCAAAATTGTGATG 2880
653 ----- 653
2881 ATTGACTCTGAATGTGCGCAAGATTCGGGGAGTTGGTGTCTGAAATTCCTCCGCGATGGCC 2940
654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
2941 AGGGACCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3000
665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
3001 GACAGCACTTCTACCGCTCACTGCTGGAGGAGATGACATGGGGACCTGTGTGATGCT 3060
685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
3061 GAGGAGTATCTGTGTACCCAGCAGCGGCTTCTCTGTCTCCAGACCTCTGCCCCGGCGCTGG 3120
705 GlyMetValHisAsnArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr 724
3121 GGCAATGTCTCCACCCAGCAGCGCTCACTACAGAGTGGCGGTGGGGACCTTGACA 3180
725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCGCCAGCTCTCCACTGGCACCCCTCCGAAGGG 3240
745 AlaGlySerAspValPheAspGlyAspLeuMetGlyAlaAlaLysGlyLeuGlnSer 764
3241 GCTGCTCCGATGATTTGATGTGACCTGGGAATGGGGCAGCCAAAGGGCTGCAAGC 3300
765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
3301 CTCCCCACATGACCCCGAGCCCTCTACAGCGGTACAGTGAGGACCCCAAGTACCCCTG 3360
785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
3361 CCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGCAGCCCCCAGCCTGATATGTG 3420
805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
3421 AACCCAGCAGATGTTCGGCCCCCAGCCCCCTTCGCCCGAGAGGGGCCCTCTGCTGCTGCC 3480
825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
3481 CGACTGTGTGTGCACCTCTGGAAGGCCCAAGACTCTCTCCCCAGGGAGAAATGGGGTC 3540
845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
3541 GTCAAGAGCTTTTTCCTTTGGCGGTGCCGTGGAGAACCCCGAGTACTTGACACCCAG 3600
865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspLeu 884
3601 GGAGGAGTGGCCCTTCAGCCCCCAGCCCTCTCTGCTTTCAGCCCCAGCCTTCCAGCAACCTC 3660
885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
3661 TATTACTGGGACCAAGACCCACAGAGCGGGGGCTCCACCAGCACCTTCAAGGGACA 3720
905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
3721 CCTACGCGCAGAGAACCCAGAGTACTCTGGTCTGGAGCTGCCAGTGTG 3765

RESULT 3

US-09-048-804-1
 ; Sequence 1, Application US/09048804
 ; Patent No. 5968748
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
 ; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 1.44 Mb diskette
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/048,804
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul K. Legard
 ; REGISTRATION NUMBER: 38,534
 ; REFERENCE/DOCKET NUMBER: ISIS-2913
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4473 base pairs
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Unknown
 ; ANTI-SENSE: No
 ; US-09-048-804-1

Alignment Scores:

Pred. No.: 0 Length: 4473
 Score: 4900.00 Matches: 919
 Percent Similarity: 73.23% Conservatives: 0
 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
 DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-09-048-804-1 (1-4473)

QY 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuAlaLeuLeuProProGlyAla 20
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 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 235 GCGAGCACCACCAAGTGTGCACCGCCGACATGAAGCTGGCGCTCTCTGCGCTCCGAG 294
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyTGlnGlyCysGlnValGlnGlnAsnLeu 60
 DB 295 ACCACCTGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAAACCTG 354
 QY 61 GluLeuThrTyThrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 DB 355 GAACTCACTTACCTGCCACCAATGCGAGCTGCTCTCTCTGCGAGGATATCCAGGAGTG 414
 QY 81 GlnGlyTyThrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuAtc 100
 DB 415 CAGGGCTACGTCTCATCGCTCAACCAAGTAGGCGAGGTCCCACTGCAGAGGCTGCGG 474
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyThrAlaLeuAlaValLeuAspAsnGly 120

DB 475 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATATGCTGCGCTGTAGACAATGGA 534
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 535 GACCCGCTGAACAATACCAACCCCTGTACAGGGGCTCCCGAGGAGCCCTGCGGGAGCTG 594
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 595 CAGCTTCGAGGCTTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 654
 QY 161 LeuCysTyThrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
 DB 655 CTCGTCTACCAAGACACGATTTGTGAGAGGACATCTTCCACAAGAACCAACCACTGGCT 714
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 DB 715 CTCACACTGATAGACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCGATGTGTAG 774
 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 775 GGCTCCCGCTGTGGGAGAGATTTCTGAGGATTTGTACAGGCTGACGCGCACTGTCTGT 834
 QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
 DB 835 GCGCGTGGCTGTGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 895 GCTGCGGCTGCACGGGCCCCAAGCACTCTGACTGCTGCGCTGCTCTCACTTCAACCA 954
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyThrAsnThrAspThrPheGlu 280
 DB 955 AGTGCACTCTGTGAGCTGCACTGCCCGCCCTGGTCACTTACAACACAGACAGTGTGAG 1014
 QY 281 SerMetProAsnProGluGlyArgTyThrPheGlyAlaSerCysValThrAlaCysPro 300
 DB 1015 TCCATGCCCAATCCGAGGGCGGTATACATTCGCGGCCAGCTGTGTGACTGTGCTGCTCC 1074
 QY 301 TyrAsnTyThrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 DB 1075 TACAACCTACTTCTACGGACGTGGGATCTGCAACCTCTGCTGCTGCTGCTGCAACCAA 1134
 QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 DB 1135 GAGGTGACAGCAGAGAGATGGACACAGCGGTGTGAGAGGTGACAGAGCCCTGTGCCCGA 1194
 QY 341 ValCysTyThrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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 DB 1255 ATCCAGAGTGTGCTGGCTGCAAGAGATCTTTGGAGGCTTGCAATTTCTGCCGAGAGC 1314
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1315 TTTGATGGGACCCAGCTCCACACTGCCCCCTCCAGCAGCAGCAGCTCCAAGTGTGT 1374
 QY 401 GluThrLeuGluGluIleThrGlyTyThrLeuTyThrIleSerAlaTrpProAspSerLeuPro 420
 DB 1375 GAGACTCTGGAAGAGATCAAGGTATACCTATATCATCTCAGCATGGCCGAGCAGCTGCT 1434
 QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
 DB 1435 GACCTCAGGCTCTTCCAGAACCTGCAGATTAATCCGGGAGCGAATTTCTGCACAAATGGCGC 1494
 QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
 DB 1495 TACTCGCTGACCTGCAAGGGCTGGCATCAGCTGGCTGGGGCTGCGCTCTCACTGAGGAA 1554
 QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480

Db 1555 CTGGGAGTGGAGCTGGCCCTCATCCACCATAAACACCACCTCTGCTTGGTGCAACCGGTG 1614
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1615 CCTGGGACCAAGCTCTTTGGAAACCGCACCAAGCTCTGCTCCACACTGGCCAAACCGGCCA 1674
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1675 GAGGACAGGTGTGTGGCGAGGGCTGGCTGCCCTGCCACCAAGCTGTGGCCCGAGGACACTGC 1734
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1735 TGGGTCCAGGGCCACCCAGTGTCTCACTGACGACAGTTCCTTCGGGGCCAGAGTGC 1794
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrpValAsnAlaArgHisCys 560
Db 1795 GTGAGGAAATGCCAGTACTGCAGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1854
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1855 TTGCCGTGCCACCTGAGTGTGACGCCCAGAAATGGCTCAGTGACCTGTGTTGGACCGGAG 1914
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Db 1915 GCTGACCAAGTGTGGCTGTGCCCACTATAGACCTCCCTTCTGGTGGCCCGCTGC 1974
Qy 601 ProSerGlyValLysProAspLeuSerTrpMetProIleTrpLysPheProAspGluGlu 620
Db 1975 CCCAGGGTGTGAAACCTGACCTCTCTACATGCCATCTGGAAGTTTCCAGATGAGGAG 2034
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 2035 GGCGCATGCCAGCTTGTGCCCATCACTGACCCACCTCCTGTGTGGAGCTGGATGACAAG 2094
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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Db 2455 CCCAAGCCAAAGAAATCTTAGAGCAAGCATACGTGATGGCTGGTGTGGGTCCCCA 2514
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Db 3055 ATTGACTCTGAATGTCCGCCCAAGATTCCGGGAGTTGGTGTCTGTAATTTCTCCGCGATGGCC 3114
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGAGCCCCAGCCCTTTGGTGCATCCAGAAATGAGGACTTGGGCCACGACGCTCTCTG 3174
Qy 665 AspSerThrPheTrpArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACTTCTACCGCTCACTCTGAGGACGATGACATGAGGGGACCTGCTGGATGCT 3234
Qy 685 GluGluTrpLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTTACCCAGCAGCGCTTCTTCTGTCAGAGCTTCCGCCCGCGCTGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerSerThrArgSerGlyGlyValAspLeuThr 724
Db 3295 GGCATGTTCACCAACAGCACCGCAGCTCATCTACAGAGTGGCGGTGGGACCTGACA 3354
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGlyGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAAGAGAGAGGCCCCCAAGGCTCTCCACTGGCACCTCCGAGGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
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Qy 785 ProSerGluThrAspGlyTrpValAlaProLeuThrCysSerProGlnProGluTrpVal 804
Db 3535 CCCTCTGAGACTGATGGCTAGCTTGGCCCTCCCTGACCTGACGCCCCCAGCCTGAAATGTG 3594
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCAGATGTTCCGGCCCCAGCCCCCTTTCGGCCCCGAGAGGGGCCCTCTGCTCTG 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTCTGGTGCCTCTGGAAGGCCCAAGACTCTCTCCCAAGGAGAGAGTGGGCTC 3714
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTrpLeuThrProGln 864
Db 3715 GTCAAGACGCTTTTGGCTTTGGGGTGGCGTGGAGAACCCCGAGTACTTGACACCCAG 3774

QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCCCACCCTCTCTCTGCTTTCAGCCAGCTTCGACACCTC 3834
QY 885 TTTTTPAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGACAGGACCCACAGCGGGGGCTCCACCCAGCACCTTCAAGGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACCTGGGCTCTGGAGCTGCCAGTG 3939

RESULT 4
US-09-056-105-26
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: KU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-26

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 3 Gaps: 1

US-09-493-480-6 (1-919) x US-09-056-105-26 (1-4473)

QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCCGGAGCC 234
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCAGGACCCCAAGTGTGCACCGGCACAGACATGAAGCTGGCGCTCCCTGCGAGTCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGTGGTGGCAGGGAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACCTACCTACCTGCCCAACATGCCAGCTGTCTCTCTGCGAGGATATCCAGGAGTG 414
QY 81 GluGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACCTGTGCTATGCTCTACACCAAGTGGAGGAGGTCCCACTGCGAGAGCTCGG 474
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCCGCTGAACAAATACACCCCTGTCTACAGGGGCTCCCGAGGAGGCTGCGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160

595 CAGCTTCGAGGCTCAGAGATCTTGAAGGAGGGTCTTGATCCAGGGAACCCCCAG 654
161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
655 CTCTGCTACAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACACACAGCTGGCT 714
181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
715 CTCACATGATAGACACCAACCGCTCTCGGGCTGACACCCCTGTTCTCGATGTGTAA 774
201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
775 GCTCCCGCTGCTGGGAGAGATTCTGAGGATTGTGAGGCTGACGCGCACTGCTGT 834
221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
835 GCGCGTGGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
895 GCTGCGGCTGCAAGGGGCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCCACAC 954
261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
955 AGTGGCATCTGTGAGCTGCACCTGCCAGGCTTGTGATCTGCTGCCCTGCCACACAA 1014
281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
1015 TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGCGCGAGCTGTGTGACTGCTGCTCC 1074
301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
1075 TACCACTACTCTTCTACGGAGCTGGGATCTGCACTCTGCTGCCCTGCCACACAA 1134
321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
1135 GAGGTGACAGCAGCAGATGCAACACAGCGGTGTGAGAGTGTGCAAGAGCCCTGTGCCCGA 1194
341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
1195 GTGTGTATGTCTGGGCTATGGAGCCTTCCGAGAGGTGAGGGCAGTTCACAGTGCCTAT 1254
361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
1255 ATCCAGAGTGTGCTGCTGCAAGAGATCTTTGGAGCTTGGCATTTCTGCCCGAGAGC 1314
381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
1315 TTTGATGGGACCCAGCTCCACACTGCCCGCTCCAGCCAGCAGCAGCTCCAAATGTGT 1374
401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
1375 GAGACTCTGGAAGAGATCACAGGTACTATACATCTCAGCATGGCGGAGCAGCTGCT 1434
421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
1435 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTCGCACAAATGGCGCC 1494
441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
1495 TACTCGCTGACCTTCAAGGCTGGGCTGAGCTGGGCTGGGCTGCTGCTGCTGAGGAA 1554
461 LeuGlySerGlyLeuAlaLeuIleHisLeuAsnThrHisLeuCysPheValHisThrVal 480
1555 CTGGGCAAGTGGAGTGGGCTCTCATCCACATAACCAACCACTCTGCTTCTGTCACAGCTG 1614
481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
1615 CCGTGGAGCAGCTCTTTGGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCA 1674
501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

1675	Db	GAGGACGAGTGTGTGGGCGAGGGGCTTGGCCCTGGCCACGACCTGTGTGGCCCCGAGGGGCACTGC	1731
521	Qy	TrpGlyProGlyPProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
1735	Db	TGGGGTCCAGGGCCACCCAGTGTGTCACTGACAGCCAGTTCTTCCGGGGCCAGGAGTGC	1794
541	Qy	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
1795	Db	GTGAGGAAATGCCAGTACTGACAGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT	1854
561	Qy	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
1855	Db	TTGCCGTGCCACCCCTGAGTGTACGCCCCAGAAATGGCTCAGTAGCCTGTTTGGACCGGAG	1914
581	Qy	AlaAspGlnCysValAlaCysAlaHisItyxIysAspProProPheCysValAlaArgCys	600
1915	Db	GCTGACCAGTGTGTGGCTGTGTGCCACTATATAGGACCCCTCCCTTCTGGGTGGCCCGGTGC	1974
601	Qy	ProSerGlyValIysProAspLeuSerTyrMetProIleTryptIysPheProAspGluGlu	620
1975	Db	CCCAGCGTGTGAACCTGCACCTCTCCTACATGCCCCATCTGGAAGTTTCAGATGAGGAG	2034
621	Qy	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspIys	640
2035	Db	GGGCGATGCCAGCCCTTCCCCCATCAACTGCACCCCACTCCTGTGTGGACCTGGATGACAG	2094
641	Qy	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
2095	Db	GGCTGCCGCCCGGAGGAGAGCCAGCCCTCTGACGTCCATCATCTCTGGGTGGTGTGGC	2154
653	Qy	-----	653
2155	Db	ATTCTGCTGCTGTGTGCTTGTGGGGTGGTCTTTGGGATGCTCTCATAGCGAGCGACGAG	2214
653	Qy	-----	653
2215	Db	AAGATCCGGAAGTACACGATGCGGAGACTGTGTCAGGAAACGGAGCTGGTGGAGCCGCTG	2274
653	Qy	-----	653
2275	Db	ACACCTAGCGGAGCGATGCCAACACGGCGCAGATGGGATCTCTGAAGAGACGGAGCTG	2334
653	Qy	-----	653
2335	Db	AGGAAGGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGCTCTACAAGGGCATCTGGATC	2394
653	Qy	-----	653
2395	Db	CCTGATGGGGAGATGTGAATAATTCAGTGGCCATCAAAGTGTGTGAGGGAAACACATCC	2454
653	Qy	-----	653
2455	Db	CCCAAGCCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA	2514
653	Qy	-----	653
2515	Db	TATGTCTCCGCCCTTCTGGGCATCTGGCTGACATCCACGGTGCAGCTGGTGACACAGCTT	2574
653	Qy	-----	653
2575	Db	ATGCCCTATGGCTGCCCTCTTAGACCATGTCCGGGAAACCGGAGCGCTGGGGCTCCAG	2634
653	Qy	-----	653
2635	Db	GACCTGCTGAACGTGGTGTATGACAGATTGCCAAGGGGATGAGCTTACCTGGAGGATGTCCGG	2694
653	Qy	-----	653
2695	Db	CTCGTACACAGGGACTTGGCCGCTCGGACGTGTGCTGTCTCAAGGTCCCAACCATGTCAA	2754
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2755	Db	ATTACAGACTTGGGGCTGGCTCGCGCTGCTGACATTCGACAGACAGAGTACTCATGCAGAT	2814

QY	653	-----	653
Db	2815	GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCCGCGCGGCTTCACC	2874
QY	653	-----	653
Db	2875	CACNAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC	2934
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Db	2935	AAACCTTACGATGGGATCCAGCCGGGAGATCCCTGCCTGTGAAAGGGGGAGCGG	2994
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Db	2995	CTGCCCGACCCCCCATCTGCACCATGTATGTCTACATGATCATGTGTCAAAATGTTGGATG	3054
QY	653	-----	653
Db	3055	ATTGACTCTGAATCTCGGCCCAAGATTCCGGGAGTTGGTGTCTGAATTCTCCCGCATGCC	3114
QY	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
Db	3115	AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCCGAGCGACTCCCTTG	3174
QY	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3175	GACAGCACCTTCTACCCCTCACTCTCGAGGAGCATCATGGGGACCTGGTGATGCT	3234
QY	685	GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyValaGly	704
Db	3235	GAGGAGTATCTGGTATCCCCAGCAGGGGCTTCTTCTGTCCAGACCTGCCCCGGGCGCTGGG	3294
QY	705	GlyMetValHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr	724
Db	3295	GGCATGGTCCACACAGGCCACCGCAGCTCATCTACCAAGAGTGGCGGTGGGACCTGACA	3354
QY	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3355	CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCGAGGCTCTCCACTGGCCACCTCCGAAGG	3414
QY	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer	764
Db	3415	GCTGGCTCCGATGTATTTGATGGTGACTCTGGGAAATGGGGGAGCCAGCAAGGGGCTGCAAGC	3474
QY	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3475	CTCCCCACATGACCCCGACCCCTCTACAGGGGTACAGTGGAGACCCCAAGTACCCCTG	3534
QY	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3535	CCCTCTGAGACTGATGGCTACGTTGGCCCTCTGACCTGCAGCCCCCAGCGCTGAATATGTG	3594
QY	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3595	AACGAGCCAGATGTTGGCCCCCAGCCCCCTTGGCCCCGAGAGGGCCCTCTGCTGCTGCC	3654
QY	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal	844
Db	3655	CGACCTCTGCTGGTGCACCTCTGGAAGAGGCCCCAGACACTCTCTCCCCAGGGGAAGATGGGGTC	3714
QY	845	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3715	GTCAAGACAGCTTTTGGCTTTGGGGGTGGCGTGGAGAAACCCCGAGTACTTTGACACCCCCAG	3774
QY	865	GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3775	GGAGGAGCTGCCCTCTAGCCCCCACCCTCTCTCTGCTCTGAGCCCCAGGCTTGCACACCTC	3834
QY	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3835	TATTACTGGGACAGGACCCACAGAGCGGGGCTCCACCCAGCACTTCAAGAGGACCA	3894

QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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Db 3895 CCTACGGCAGAGAACCCAGGTACCTGGGTCTGGAGTCCCGAGTG 3939

RESULT 5

US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)...(3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-663-834A-3 (1-4473)

QY 1 MetGluLeuAlaAlaLeuCysAArgTTPGlyLeuLeuAlaLeuLeuProGlyVala 20
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Db 175 ATGAGCTGGCGGCTTGTGGCGCTCTCTGGCGCTCTCTGGCGCTCTCTGGCGGAGCC 234
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
|||||
Db 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGTGGCGCTCTCTGGCGGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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Db 295 ACCACCTGGACATGCTCCGCCACCTCTACACAGGCTGCCAGGTGTGCAGGGGAAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspLeuGlnVal 80
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Db 355 GAACCTCACCTTACCTGCCCAATGCCAATGCCAGCTGTCTCTCTGCAGATATCCAGGAGTG 414
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
|||||
Db 415 CAGGGCTACGTGTCTATCGCTCACACCAAGTGCAGCGAGGTCCCACTGCAGAGGCTGCGG 474
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
|||||
Db 475 ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATGCTCCCTGGCGGTGTAGCAATGGA 534
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
|||||
Db 535 GACCCGCTGAACAAATACCACTCTGTCAAGGGGCTCTCCACAGAGGCTGTCCGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuLeuLeuGlnArgAsnProGln 160
|||||
Db 595 CAGCTTCGAGCTCTACAGAGATCTTGAAGAGGGGTCTTGTATCCAGCGGAACCCCGCAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuThrPlyAspIlePheHisLysAsnAsnGlnLeuAla 180
|||||
Db 655 CTCTGCTACCGAGACAGCAATTTTGTGAAGGACATCTTCCACAGAACCAACCAAGCTGGCT 714
QY 181 LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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Db 715 CTCACACTGATAGACACCAACCGCTCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG 774
QY 201 GlySerArgCysTyrPglyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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Db 775 GGCCTCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTACAGAGCTTGACGCGCACTGCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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Db 835 GCGGTGGCTGTGCCCGCTGCAGAGGGCCACTGCCCACTGACTGCTGCTGCCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Db 895 GCTGCGGCTGCACAGGGCCCCAAGCACTCTGACTGCTGCTGCTGCTCTCCACTTCAACCA 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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Db 955 AGTGGCATCTGTGAGCTGCACCTGCCAGGCCCTGTGTCACCTACCAACACAGACACGTTT 1014
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Db 1015 TCCATGCCCAATCCCGAGGGCCGATATACATTGCGCGCCAGCTGTGTGACTGCTGCTCCC 1074
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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Db 1075 TACAACCTACCTTTCTAGCGAGCTGGGATCTCTGCACCTCTGCTGCGCCCTGCACACCAA 1134
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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Db 1135 GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAGGTGCAGCAAGCCCTGTGCCCGGA 1194
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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Db 1195 GTGTCTATGCTGTGGGCATGGAGCACTTCCGAGAGGTGAGGGCAGTTACCACTGCCAAT 1254
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
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Db 1255 ATCCAGAGTTTCTGCTGCTGCAAGAGATCTTTGGGAGCCCTGGCATTTCTGCGGAGAGC 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe 400
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Db 1315 TTTGATGGGGACCCAGCCCTCCAACTGCCCCCTCCAGCAGCAGCAGCTTCAAGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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Db 1375 GAGACTCTGGAGAGATTCACAGGTACCTATACATCTCAGCATGGCCGAGCAGCTGCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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Db 1435 GACCTCAGCGCTCTTCCAGAACCTGCAAGTAAATCCGGGACGAAATTCGCAATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
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Db 1495 TACTCCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGAA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
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Db 1555 CTGGGCACTGGACTGGCCCTCATCCACATAACACCCACCTCTGCTTCTGTCACACGCTG 1614
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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Db 1615 CCCTGGGACCCAGCTCTTTCCGAAACCCCGACACAGCTCTGCTCCACACTGCCAACCGGCA 1674
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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Db 1675 GAGGACAGTGTGTGGGGAGGGGCTTGGCTCTGCCACCACTGTGCGGCCCGGAGGACCTGC 1734
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
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Db 1735 TGGGTCACGGGCCACCCAGTGTGTCACTGCAGCCAGTTCCTTCCGGGGCAGGAGTGC 1794
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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Db 1795 GTGGAGAAATGCCGAGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1854

Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1855 TTGCGGTGCCACCTGAGTGTGAGCCCGCAGAAATGGCTCAGTGACCTGTTTGGACCGGAG 1914
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProProPheCysValAlaAspCys 600
Db 1915 GCTGACGAGTGTGGGCTGTGGCCACATATAGAGACCTCCCTTCTGCGTGGCCGCTGC 1974
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
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Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
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Qy 641 GlyCysProAlaGluGlnAlaAspLeuThrSer 653
Db 2095 GGCTGCCCCCGGAGAGAGAGCCAGCCCTCTGACGTCCTATCATCTCTGCGGTGGTGGC 2154
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Db 2215 AAGATCGGAAGTACACGATCGGAGACTGTGCGAGAAACGGAGCTGTGTGGAGCGGCTG 2274
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Db 2275 ACACCTAGCGGAGCGATGCCCAAACGAGCGCAGATGCGGATCTCTGAAAGAGACGAGCTG 2334
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Qy 654 654
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Qy 665 AspSerThrPheTyrArgSerLeuLeuAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACTTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGTGTGGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGGTACCCAGCAGCGCTTCTTCTGTCCAGACCTGCCCCGCGCGCTGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGCATGGTCCACCAAGCAGCGCAGCTCATCTACGAGAGTGGCGGTGGACCTCGACA 3354
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGCTGGAGCCCTCTGAAGAGAGGCGCCCGCAGGTCTCCACTGGCACCTCTCGAAGGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
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Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
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Db 3595 AACCAGCAGATGTTGGCCCCAGCCCCCTTCCGCCCGAGAGGGGCTCTGCTGCTGCTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGTGTGGCTCACTCTGGAAGGGCCCAAGACTCTCTCCCGAGGGAAGATGGGGTC 3714
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAAGACGTTTTCCTTTGGGGGTGCTGGTGGAGAACCCCGAGTACTTGACACCCAG 3774
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCCAGCCCCCTCTCTCTGCTTTCAGCCAGCCCTTCGACACACCTC 3834
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACCCAGGACCCACAGAGCGGGGGCTCCACCCAGGACCTTCAAGGGACA 3894
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTTGGAGGTGCCAGTGT 3939

RESULT 6

US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:

; APPLICANT: Erickson, Sharon
 ; APPLICANT: Schwall, Ralph
 ; APPLICANT: King, Kathleen
 ; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
 ; FILE REFERENCE: GENENT.034A
 ; CURRENT APPLICATION NUMBER: US/09/811,115
 ; CURRENT FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/189,844
 ; PRIOR FILING DATE: 2000-03-16
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-811-115-2

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 4892.00 Matches: 918
 Percent Similarity: 73.15% Conservative: 0
 Best Local Similarity: 73.15% Mismatches: 1
 Query Match: 96.34% Indels: 336
 DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-2 (1-3768)
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 DB 1 ATGGAGCTGGCGGCTTGTGGCGCTGGCGGCTCTCTCGCCCTCTTGGCCCCCGAGCC 60
 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 61 GCGAGCACCAAGTGTGACCGCCGACAGACATGAGCTGCGGCTCTCTCGCCAGTCCCGAG 120
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 121 ACCCACTGGAGATGCTCGGCACCTCTACCGAGGCTGCGAGTGTGCGGGAACCTG 180
 QY 61 GluLeuThrTyrluProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 DB 181 GAACCTACCTACTGCTCCCAATGCGAGCTGTCTCTCTGCGAGTATCCAGGAGGTG 240
 QY 81 GlnGlyTyrluValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 241 CAGGGCTACGTGCTCATCGCTCAACCAAGTGTGAGCGAGTCCCACTGCGAGGCTGCGG 300
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrluAlaLeuAlaValLeuAspAsnGly 120
 DB 301 ATTGTGCGAGGCAACCGAGCTCTTTGAGGACACTATGCTGCGCTGCTGCTGAGACAATGA 360
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 361 GACCCGCTGAACAATACCACTCTGTCAGAGGCTCTCCCGAGGAGGCTGCGGAGCTG 420
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 421 CAGCTTCGAGGCTCACAGAGATCTTGAAGAGACATCTTCCACAGAACCAACAGCTGGCT 480
 QY 161 LeuCysTyrluGlnAspThrIleLeuTyrluAspIlePheHisLysAsnGlnLeuAla 180
 DB 481 CTCTGCTACCGAGACAGATTTGTGAAGAGACATCTTCCACAGAACCAACAGCTGGCT 540
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 DB 541 CTCACACTGATACACCAACCGCTCTCGGGCTGCGCCCTGCGCCCTGCTCCGATGTGTAA 600
 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 601 GGCTCCCGCTGCTGGGAGAGAGTCTGAGGATTTGTGAGGCTGAGAGCTGAGCGCACTGTCT 660
 QY 221 AlaGlyGlyCysAlaArgCysGlyProLeuProThrAspCysCysHisGlnGlnCys 240

DB 661 GCCGCTGGCTGTGCCCGCTGCAAGGGGCGCACTGCCCACTGACTGCTGCCATGAGCAGTGT 720
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 721 GCTGCCGCTGCACCGGCGCCCAAGCACTGTGACTGCTGGCTGCTCCACTTCAACCCAC 780
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrluAsnThrAspThrPheGlu 280
 DB 781 AGTGGCANTCTGTGAGCTGCACTGCCCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 281 SerMetProAsnProGluGlyArgTyrluPheGlyAlaSerCysValThrAlaCysPro 300
 DB 841 TCCATGCCCAATCCCGAGGCGGTATACATTCGGCGCGCAGCTGTGTGCTGCTGCTGCC 900
 QY 301 TyrluAsnTyrluSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 DB 901 TACAATACCTTTCTACGAGCGTGGATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 DB 961 GAGGTGACAGCAGAGAGATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCTGTGCCCG 1020
 QY 341 ValCysTyrluGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 DB 1021 GTGTGCTATGTGCTGCGGCAATGGAGCACTTGGCGAGAGTGTGAGGCGAGTACCA 1080
 QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 DB 1081 ATCCAGGAGTGTGCTGGCTGCAAGAGATCTTTGGGAGCTGCGATTTCTGCCGAGAGC 1140
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1141 TTTGATGGGACCCAGCCTCCAACTGCTCCCGCTCCAGCCAGCAGCAGCTCCAA 1200
 QY 401 GluThrLeuGluGluIleThrGlyTyrluTyrluIleSerAlaValProAspSerLeuPro 420
 DB 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATATCTCAGCATGTGGCGGCGAGCGCTGC 1260
 QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala 440
 DB 1261 GACCTCAGCGCTTTCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACATGGGCG 1320
 QY 441 TyrluSerLeuThrLeuGlnGlyLeuGlyIleSerTyrluLeuArgSerLeuArgGlu 460
 DB 1321 TACTGCTGACCTGCAAGGCTGGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1380
 QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
 DB 1381 CTGGGAGTGTGAGTGTGCGCTCTCAACCACTTAACCACTGCTGCTGCTGCTGCTGCTG 1440
 QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 DB 1441 CCTGGGAGCAGCTCTTTGGGAACCCCGACCAAGCTCTGCTCCACACTGCTCCACCGG 1500
 QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 DB 1501 GAGGACAGTGTGTGGCGGAGGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 1560
 QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
 DB 1561 TGGGCTCCAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
 QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGlyTyrluValAsnAlaArgHisCys 560
 DB 1621 GTGGAGGAATGCGAGTGTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTG 1680
 QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
 DB 1681 TTGCGCTGCCACCTGAGTGTGAGCGGCGGCGGCTGCGGCGGCTGCGGCGGCTGCG 1740
 QY 581 AlaAspGlnCysValAlaCysAlaHisTyrluAspProPheCysValAlaArgCys 600
 DB 1741 GCTGACGAGTGTGCGGCTGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCT 1800

Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleThrLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGTAACCTGACCTCTCCACATGCCCCTCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GGCGCATGCCAGCTTGGCCCCATCACTGACCCACTCTCTGTGGACTGTGATGACAAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGAGTCCATCTCTCGGTGGTTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCGTGCTGCTGTCTTGGGGTGTGTTTGGGATCTCTCATCAAGCAGCGAGCAG 2040
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Qy 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATGCCGATCCTGAAAGAGCGAGCTG 2160
Qy 653 ----- 653
Db 2161 AGGAAGTGAAGTGTCTGGATCTGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2220
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Db 2221 CCTGATGGGAGAAATGTGAAATTCAGTGGCCATCAAAGTGTGAGGGAACACATCC 2280
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Qy 653 ----- 653
Db 2401 ATGCCCTATGCTGCTCTTAGACCATGTCCGGGAAACCGCGAGCGCTGGGCTCCAG 2460
Qy 653 ----- 653
Db 2461 GACCTGCTGAATGCTGTATCGAGTTGCCAAGGGGATGACTACCTGGAGGATGTGGG 2520
Qy 653 ----- 653
Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACTGTGCTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTGGGCTGGCTGGCTGTGGACATTTGACGAGACAGAGTACCATGACAT 2640
Qy 653 ----- 653
Db 2641 GGGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAGTCCATCTTCGCGCGGCTTACCC 2700
Qy 653 ----- 653
Db 2701 CACCAGAGTGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACTGCTGGAAAGGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTTCAATGTTGGATG 2880

Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGGCAAGATTCCGGAGATGGTGTCTCGAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTTGTGTGTCATCCAGATGAGGACTTGGGCCCGAGCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTCTACCGCTCACTGCTGGAGGACGATGATCGGGGACCTGTGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTATCCCGCAGCAGGGCTTCTCTGTCTCCAGACCTCTGCCCGCGCTGGG 3120
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACCACGAGCAGCCGAGCTCTTACCGAGGAGTGGCGGTGGGACCTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCTGGAGCCCTCTGAAGAGAGGCGCCCGAGTCTTCCACTGGCACCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGTATTTGATGGTGACCTTGGGAATGGGGGCGAGCCAAAGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACACATGACCCCGAGCCCTCTACAGCGGTACAGTGGAGACCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGCAGCCCCCAGCTGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCAGATGTTGGCCCCCGAGCCCTTGTGCCCGAGAGGGGGCTCTGTGCTGTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACTGTGTGTGCACTCTGGAAGGGCCAGACTCTCTCCAGGGAGAGATGGGGTTC 3540
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCTTTTGTGCTTGGGGTGGCGTGGAGAACCCCGAGTACTTGACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspLeu 884
Db 3601 GGAGGAGTGGCCCTCAGCCCCACCTCTCTGTGCTTTCAGCCCCAGCTTCGACACCTC 3660
Qy 885 TyrTyrTyrAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGACACAGGACCCACAGAGCGGGGGCTTCCACCCGAGCACCTTCAAGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGCGAGAGAACCCAGAGTACCTGGGTCTGGAGCTGCCAGTG 3765

RESULT 7

US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARFAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200

CITY: Atlanta
 STATE: Georgia
 COUNTRY: usa
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/229,515A
 FILING DATE: 19 APR 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PERRYMAN, DAVID G
 REGISTRATION NUMBER: 33,438
 REFERENCE/DOCKET NUMBER: 1414.608
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-688-0770
 TELEFAX: 404-688-9880
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4530 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-229-515A-9

Alignment Scores:
 Pred. No.: 0 Length: 4530
 Score: 4892.00 Matches: 918
 Percent Similarity: 73.15% Conservative: 0
 Best Local Similarity: 73.15% Mismatches: 1
 Query Match: 96.34% Indels: 336
 DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-229-515A-9 (1-4530)

181	leuThrLeuIleaspThrAspArgSerArgAlaCysHisProCysSerProMetCysAla	200
691	CTCACATGATAGACACCAACCGCTCTCGGGCGCTGCACCCCTGTTCTTCGATGTGTAA	750
201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
751	GGCTCCCGCTGCTGGGGAGAGATTCTGAGGATTGTTCAGAGCCTGACGGCACA	810
221	AlaGlyGlyCysAlaArgCysGlyProLeuProThrAspCysCysHisGluGlnCys	240
811	GCCTGGCTGCTGCTCCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	870
241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
871	GCTGCCGGCTGCAGGGCCCCAAGCACTCTGACTGCTGGCTGCTCTCACTTCAACAC	930
261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
931	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACCTACCAACACAGACAGTGTGAG	990
281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
991	TCCATGCCCAATCCCGAGGGCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTCCC	1050
301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
1051	TACAACTACCTTTCTACGGAGCTGGGATCCTGCACCTCTGTGCCCTCTGCACACCA	1110
321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
1111	GAGGTGACAGCAGAGGATGGACACAGCGGTGTGAGAAGTGCAGCAAGCCTCTGTGCCGA	1170
341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
1171	GTGTGCTATGCTCTGGGCATGGAGCACTTTCGAGAGGTGTGAGGCGAGTTACCACTGCCA	1230
361	IleGlnGluPheAlaGlyCysValLeuPheGlySerLeuAlaPheLeuProGluSer	380
1231	ATCCAGAGGTTTGTGGCTGCAAGAGATCTTTGGAGGCTTGCATTTCTGCCGAGAGC	1290
381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
1291	TTTGATGGGACCCAGCCTCCAACTGCCCCGCTCCAGCAGCAGCAGCTCCAAGTGT	1350
401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
1351	GAGACTCTGGAAGAGATCAAGGTTACCTATATCATCTCAGCATGGCGGACAGCCTGCCT	1410
421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
1411	GACCTCAGCGCTCTTCAGAACCTTGCAAGTAAATCCGGGGACGAATTTCTGCACATGGGCC	1470
441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
1471	TACTCGTCACTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTGAGGGA	1530
461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
1531	CTGGGAGTGGAGTGGCTCTCATCCACCAATACACCCACCTCTGCTCTGTCGACACCGGT	1590
481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
1591	CCCTGGGACAGCTCTTTGGAAACCCGACCAAGCTCTGCTCCACACTGTCACACCGGCCA	1650
501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
1651	GAGGACAGTGTGTGGGGGAGGCGCTGGCGCTGCACCGCTGTGGCGCCGAGGCGCACTGC	1710
521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
1711	TGGGGTCCAGGGGCCCAACCCAGTGTGTCACTGAGCCAGGTTCTTCTCGGGGCGCAGAGTGC	1770

QY 541 valGluGluCysArgValLeuGlnGlnGlyLeuProArgGluTyrValAsnAlaAraGHisCys 560
DB 1771 GTGGAGAAATGCCAGTACTGCGAGGGCTCTCCAGGGAGTATGTAATGCCAGGCACTGT 1830
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1831 TTGCGGTGCCACCTGAGTGTGAGCCCGCCAGATGGCTCACTGACCTGTCTTTGGACCGGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProProPheCysValAlaAraGHisCys 600
DB 1891 GCTGACCAAGTGTGGCTGTGGCCCACTATAAGAGACCTCCCTTCTCGTGGCGCGCTGC 1950
QY 601 ProSerGlyValIlyAspProAspLeuSerTyrMetProIleTyrPhePheProAspGluGlu 620
DB 1951 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 2011 GGGCGATGCCAGCTTGGCCCATCACTGACCCACTCTCTGTGTGGACCTGGATGACAAG 2070
QY 641 GlyCysProAlaGluGlnAraGAlaSerProLeuThrSer 653
DB 2071 GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATGCTCTCTGGGGTGGTGGC 2130
QY 653 ----- 653
DB 2131 ATTCTGCTGCTGCTGCTTGGGGTGGTCTTTGGGATCTCTCATCAAGCGACGGCAG 2190
QY 653 ----- 653
DB 2191 AAGATCGGAAGTACAGATGCGGAGACTGCTGCGAAGACGGAGCTGGTGGAGCCGCTG 2250
QY 653 ----- 653
DB 2251 ACACCTAGCGGAGCGATGCCCAACCGAGCGATGCGGATCTCTCAAGAGACGGAGCTG 2310
QY 653 ----- 653
DB 2311 AGGAAGTGAAGTGTCTGGATCTGGCGCTTTTGGGCACAGTCTTCAAGGGCATCTGGATC 2370
QY 653 ----- 653
DB 2371 CCTGATGGGGAGATGTGAATAATTCAGTGGCCATCAAGTGTGAGGAAAAACACATCC 2430
QY 653 ----- 653
DB 2431 CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGGCTCCCA 2490
QY 653 ----- 653
DB 2491 TATGCTCTCCGCTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2550
QY 653 ----- 653
DB 2551 ATGCCCTATGCTGCTCTTAGACCATGTCCGGGAAACCGGAGACGCTGGGCTCCAG 2610
QY 653 ----- 653
DB 2611 GACCTGTGAATGCTGTATGCAATGTCGAAGGAGTACCTACCTGGAGGATGTGCGG 2670
QY 653 ----- 653
DB 2671 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGATCAAGTGTCAAGATGCCAATGTCAA 2730
QY 653 ----- 653
DB 2731 ATTACAGACTTGGGCTGGCTCGGCTGTGACATTTGACGACAGATGACCATGTCAGAT 2790
QY 653 ----- 653
DB 2791 GGGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAGTGCATTTCTCCGCGCGGCTTACCC 2850
QY 653 ----- 653

RESULT 8

US-08-645-865-9

DB 2851 CACCAGAGTGTGTGTGGAGTTATGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2910
QY 653 ----- 653
DB 2911 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGGGGGAGCGG 2970
QY 653 ----- 653
DB 2971 CTGCCCCAGCCCCCATCTGTGACCAATTGATGTCTACATGATCAATGGTCAATTTGGATG 3030
QY 653 ----- 653
DB 3031 ATTGACTCTGAATGTCCGCCAAGATTCCGGAGTTGGTGTCTGAATTTCTCCCGCATGCC 3090
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 3091 AGGACCCCCAGCCCTTTGTGTCTATCCAGAAATGAGGACTTGGGCCCGACGATCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
DB 3151 GACAGCACCTTCTACCCGCTCACTGTGGAGACGATGATGGGGACTGTGTGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3211 GAGGATATCTGGTATCCCGACGAGGGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGG 3270
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
DB 3271 GGCAATGCTCCACACAGCACCGCAGCTCTATACAGAGTGGCGGTGGGGACCTTGACA 3330
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DB 3331 CTAGGGTGGAGCCCTCTGAAGAGAGGCCCCCAGGTCTCCACTGGCACCTCCGAGGG 3390
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
DB 3391 GCTGGCTCCGATGATTTGATGTGTGACTGGGAATGGGGCAGCAAGGGCTGCAAGC 3450
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
DB 3451 CTCCCCACATGATCCCGACCCCTCTACAGCGGTACAGTGGAGACCCACACATACCCCTG 3510
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlyVal 804
DB 3511 CCCTCTGAGACTGATGGCTAGTGTGCCCTCCCTGACCTGACGCCCGCCAGCTGATATGTG 3570
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
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QY 825 ArgProAlaGlyAlaThrLeuGluArgProIlySerThrLeuSerProGlyIlyAsnGlyVal 844
DB 3631 CGACCTGTGTGTGCACTCTGGAAGGGCCAGGACTCTCTCCCGAGGAAGAAATGGGGTC 3690
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QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
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DB 3871 CCTACGGCAGAGAACCCAGAGTACTCTGGGTCTGGACACGTGCCAGTG 3915

Sequence 9, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARAKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-645-865-9

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservativeness: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-645-865-9 (1-4530)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla 20
DB 151 ATGGAGCTGGCGGCTTGTGGCGCTGGGGGCTCTCTCGCCCTCTTGGCCCCCGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCGAGACCCCAAGTGTGACCGGCGACAGATGAGCTGGGCTCTCTCGAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCACCTGGACATGCTCCGCCACCTCTACCGGGCTGCCAGTGTGTGCGAGGAACCTG 330
QY 61 GluLeuThrTyrlenProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 331 GAATCACCCTACCTGCGCCACCAATGCGAGCTGTCTCTCGAGGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrlenValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTAGCTGCTATCGCTCAACAACCAAGTGGAGCGAGTCCCACTGCGAGGCTGCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrlaLeuAlaValLeuAspAsnGly 120
DB 451 ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCTGCGCTGGCGCTGCTAGACATGGA 510

QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCCCCAGGAGGCTGGGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
DB 571 CAGCTTCGAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCAG 630
QY 161 LeuCysTyrlenAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
DB 631 CTCTGCTACCAAGACACGATTTGTGAAGGACATCTTCCACAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCTCGATGTGTA 750
QY 201 GlySerArgCysTrpGlyLysSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTTCTGAGGCTTGACGGCCTGCTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 811 GCCGTGGCTGTGCCCGCTGCAAGGGGCGACTGCCACTGCTGCTGCCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGACCGGGCCCCAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrlenAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990
QY 281 SerMetProAsnProGluGlyArgTyrlenPheGlyAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCCAATGCCGAGGCGCGGTATACATTCGGGCGCGAGCTGTGTGCTGCTGCTG 1050
QY 301 TyrAsnTyrlenLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1051 TACAACCTACTTCTACGAGCTGGGATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1231 ATCCAGGAGTTTGTGGCTGCAAGAGATCTTGGGAGCTGSCATTTCTGCCGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe 400
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QY 401 GluThrLeuGluGluIleThrGlyTyrlenTyrlenIleSerAlaTrpProAspSerLeuPro 420
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QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1471 TACTCGCTGACCTGCAAGGGCTGGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1530
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1531 CTGGGCGAGTGGAGTGGCCCTTCATCCACCAATACCCACCTCTGCTGCTGCTGCTGCTG 1590
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500

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1711 TGGGGTCCAGGGCCACCCAGTGTCAACTGCAGCCAGTTCCTTCGGGGGCCAGGAGTGC 1770
Qy ValGluGluCysAArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAArgHisCys 560
1771 GTGAGGAGATCCCGAGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACCTGT 1830
Qy LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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Qy AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProPheCysValAlaAArgCys 600
1891 GCTACCAAGTGTGGGCTGTGGCCCTATTAAGACCCCTCCCTTCGCGTGGCCCGCTGC 1950
Qy ProSerGlyValIlyAspLeuSerTyrMetProIleTyrIlyAspPheProAspGluGlu 620
1951 CCCAGCGGTGGAACCTGACCTCTCTACATGCCCACTCTGGAAGTTCACAGATGAGGAG 2010
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2011 GGCAGATGCCAGCTTGGCCCATCACTGACCCCACTCTCTGTGTGGACCTGGATGACAAG 2070
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Qy 653 ----- 653
2131 ATTCTGTGTGTGTGTGTGTGGGGTGTCTTTGGGGTCTCTATCAAGCGACGGAGCG 2190
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Db 3031 ATTGACTCTGAATGTGCGCCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3090
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Db 3091 AGGGACCCCGAGCGCTTTGTGTCTATCCAGAATGAGGACTTGGGGCCAGCCAGTCCCTTG 3150
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
3151 GACAGACCTTTCTACCGCTCACTGCTGGAGACGATGATGATGGGAGCTGTGTGATGCT 3210
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
3211 GAGGAGTATCTGTATCCCGCAGCAGGCTTCTTGTCTCAGACCTTGTCCCGCGCGCTGG 3270
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
3271 GGCATGTGTCCACCAAGCACCGCAGCTCATCTACAGAGTGGCGGTGGGACCTTGACA 3330
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
3331 CTAGGCTGTGAGCCCTCTGAAGAGAGGAGCCCGCAGGTCTCCACTGGCACCTCCGAGGG 3390
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
3391 GCTGGCTCCGATGTATTTGATGGTACCTGGGAATGGGGAGCCAGCCAGGGGCTGCAAGC 3450
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
3451 CTCCCCACACATGACCCCGCAGCTCTACAGCGGTACAGTGGAGACCCCACTACCCCTG 3510
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
3511 CCCTCTGAGACTGATGGCTAGCTTGGCCCTCCCTGACCTGAGGAGCCCGAGGCTGATATGTG 3570
Qy 805 AsnGlnProAspValArgProGlnProSerProArgGluGlyGluProLeuProAlaAla 824
3571 AACCCAGCAGATTTGGCCCGCAGCCCTTCCCGCCGAGAGGGGCTCTGCTGTGCTGCC 3630
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProIlySerThrLeuSerProGlyLysAsnGlyVal 844
3631 CGACCTGTGTGGCTCACTCTGGAAGGGCCCAAGACTCTCTCCCGAGGGGAAGTGGGGTC 3690
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
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QY 885 TTTTtTtPAspGlnAspProProGluArgGlyAlaProProSerThrPhelysGlyThr 904
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RESULT 9

US-09-167-322-4
; Sequence 4, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seigel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998

CLASSIFICATION DATA:
; APPLICATION NUMBER: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
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INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-167-322-4

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-167-322-4 (1-4530)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCAGTGTGCACCGGCACAGACATGAAGCTGGGGCTCCCTGCCAGTCCCGGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60

Db 271 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCAGGTGGTGCAGGGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnPheLeuVal 80
Db 331 GAACTCACCTACCTGCTCCCAATGCAGCTGTCTCTCTGCAGGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTCTCATCGCTCACACCAAGTGAGCGAGTCCCTACCTGCAGAGGCTCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTTGGCGAGGACCCAGCTCTTTGAGGACCACTATGCTCCCTGGCGCTGTAGCAATGGA 510
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QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuGlnArgAsnProGln 160
Db 571 CAGCTTCGAGGCTTCACAGAGATCTTGAAGGAGGGCTCTTGATCCAGCGGAACCCCGAG 630
QY 161 LeuCysTyrGlnAspThrLeuLeuTrpLysAspPheHisLysAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACAGGACACGATTTTGTGGNAGGACATCTTCCACAAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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Db 751 GGCTCCCGCTGCTGGGGAGGAGATTCTGAGGATTGTACAGAGCTTGACGCGCACTGTCT 810
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Db 811 GCGGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCACTGCTGCTGCCATGACAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 261 SerGlyValCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGTGTCACTTACACACAGACACGCTTGAG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Db 1051 TACAACCTACCTTTCTACGGAGCTGGGATCTCTGCACCCCTCTGCTGCCCTTCGCACACAA 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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Db 1231 ATCCAGGAGTTTGTGCTGCGAGAGAGATCTTTGGGAGCTTGGCATTTCTGCGGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1291 TTTGATGGGACCCAGGCTCCACACTGCCCCGCTCCAGCGCAGAGCAGCTCCAAGTGTGT 1350
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420

Db	1351	GAGACTCTGGAAGAGATCA	CAGGCTTACCTATACATCTCAGCATGTGGCCGACAGCCTGCGCT	1411
Qy	421	AspLeuSerValPheGlnAsnLeuGlnVal	lleArgGlyArgIleleuHisAsnGlyAla	440
Db	1411	GACCTCAGCGCTCTCCAGAACCTGCAAGTAATCCGGGGACGAAATCTGCACAAATGGCGCC	1470	
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	
Db	1471	TACTCGCTGACCTCGCAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGTGAGGGAA	1530	
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480	
Db	1531	CTGGCAGTGGACTGGCCCTCATCCACCAATAACACCCACTCTGCTTCTGTGCACACGGTG	1590	
Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	
Db	1591	CCCTGGGACCAGCTCTTTTGGAAACCCGCAACAGCTCTGCTCCACACTGCCAACCCGCGCA	1650	
Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	
Db	1651	GAGGACGAGTGTGTGGCGGAGGCGCTGGCTGCCACCCAGCTGTGCGCCGAGGCGACTGC	1710	
Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	
Db	1711	TGGGGTCCAGGGGCCACCCAGTGTGTCAACTGCAGCCAGTCTCTTCGGGGCCAGGAGTGC	1770	
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	
Db	1771	GTGGAGGAATGCCGAGTACTTGCAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT	1830	
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	
Db	1831	TTGCGGTGCCACCTCGAGTGTGAGCCCCAGATGGCTCAGTGACTGTTTGTGACCGGAG	1890	
Qy	581	AlaAspGlnCysValAlaCysAlaHisGlyIleAspProProPheCysValAlaArgCys	600	
Db	1891	GCTGACCAGTGTGTGGGCTGTGGCCCACTATAAGSACCCCTCCCTCTCTCGTGGGCCCGCTGC	1950	
Qy	601	ProSerGlyValIysProAspLeuSerTyrMetProIleTrpIysPheProAspGluGlu	620	
Db	1951	CCGAGCGGTGTGAACCTGACCTCTCTCATATGCCCACTTGGAAAGTTTCCAGATGAGGAG	2010	
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640	
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Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653	
Db	2071	GGCTGCCCCCGCAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTCGGTGGTTGGC	2130	
Qy	653	-----	653	
Db	2131	ATTCTGCTGTGTGTCTTGGGGGTGGTCTTTTGGGATCTCATCAGCGACCGGACGAG	2190	
Qy	653	-----	653	
Db	2191	AAGATCCGGAAGTACAGATGCGGAGACTGCTGCAGGAAACGGAGCTGTGTGGAGCCGCTG	2250	
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Db	2311	AGGAAGTGAAGGTCTTGGATCTGGCGCTTTTGGCAGCTCTACAGGGCATTCTGGATC	2370	
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Db	2971	CTGCCCCAGCCCCCATCTGCAACATTGATGTCTACATGATCATGTGTCAAAATGTTGGATG	3030
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Qy	665	AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3151	GACAGCACCTTCTACCCGCTCACTGCTCGAGGACGATGACATGGGGHACCTGTGTGGATGCT	3210
Qy	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProIlaProGlyAlaGly	704
Db	3211	GAGGAGTATCTGGTATCCCGACGAGGGCTTCTTCTGTCCAGACCTGTGCCCGGGCGCTGGG	3270
Qy	705	GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr	724
Db	3271	GGCATGGTCCACCAACAGGCAACCGCAGCTCATCTACACAGGAGTGGCGGTGGGACCTGACA	3330
Qy	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3331	CTAGGGCTGGAGCCCTCTGAGAGGAGGCCCCCAGAGTCTCCACTGGCACCTCCGAAGGG	3390
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaIalalyGlyLeuGlnSer	764
Db	3391	GCTGGCTCCGATGTATTGTATGGTGAUCTGGGAATGGGGGACGCAAGGGGCTGCAAAAGC	3450
Qy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3451	CTCCCCACACATGACCCGCTCTACAGGGGTACAGTGGAGNACCCACAGTACCCCTG	3510
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3511	CCCTCTGAGCTGATGCTACCTTGGCCCCCTGACCTGACGCCCCACGCTGATATGTG	3570

Db 3691 GTCAAGACGTTTGTGGGCTGGCGGAGAAACCCGAGTACTTGACACCCCGAG 3750
Qy GlyGlyAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3751 GGAGAGCTGCCCTCAGCCACCCCTCTCTGCTTTCAGCCGAGCTTCGACACCTC 3810
Qy TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheGlyThr 904
Db 3811 TATTACTGGACAGGACCCAGACCCAGAGCGGGGGCTCCACCCAGCACCTTCAGAGGGACA 3870
Qy ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3871 CCTACGGCAGAGAACCCAGAGTACTGGGCTCGGACGTGCCAGTG 3915

RESULT 11

US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-877-177A-11 (1-4530)

Qy 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 151 ATGGAGCTTGGCGGCTTGTGCGCTTGGGGCTCTCTCGCCTCTTGCCCGCGAGCC 210
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCAAAGTGTGCACCGGCACACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 270
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCCACTGGACATCTCGGCACCTCTACACAGGGCTGCGAGGTGGTGGAGGAAACCTG 330
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 331 GNACTCACTACTGCGCCACCACTGCGAGCTGCTCTTCTGACGATATCCAGGAGGTG 390
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTGCTCATCGCTCACCAACCAAGTGGAGGAGGTGCCACTGCGAGGGCTGCGG 450
Qy 101 IleValArgGlyThrGlnPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGCTGACAAATGGA 510
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAATACCAACCTTGTTCACAGGGGCTCCCGAGGAGGCTGCGGAGCTG 570

Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgSerProGln 160
Db 571 CAGCTTCGAAACCTCACAGATCTTGAAGAGAGGGTCTTGATCCAGCGGAACCCCGAG 630
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLeuAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACAGGACAGATTTTGTGGAGAGNACATCTTCCACAGNACAAACAGCTGGCT 690
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAG 750
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GGCTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTGTGAGAGCTTCAGAGCTTCAGCGGCACTGCTGT 810
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 811 GCGGTGCTGTGCTGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 870
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTGCCGCTGCACGCGGCCCAAGCACTCTGACTGCTGCTGGCTGCTCCACTTCAACCCAC 930
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTCAACACACAGACAGTTTGAG 990
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTCCC 1050
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1051 TACAACCTACTTCTACGAGCTGGGATCTGACACCTCTGCTGCTGCCCTGCAACACCAA 1110
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1111 GAGGTGACAGCAGAGAGATGGAAACACAGCGGTGTGAGAGTGGACNAGCCCTGTGCCCGA 1170
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1171 GTGTCTATGCTCTGGGCATGGAGCACTTCGAGAGGTGGAGGCACTTACCAGTGCAT 1230
Qy 361 IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGGAGTTTGTGCTGGCTGCAAGAAGATCTTTTGGAGGCTGGCATTTCTGCCGAGAGC 1290
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1291 TTTGATGGGGACCCAGCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCAGTGTGT 1350
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1351 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGCGCGAGACGCTGCT 1410
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnGlyAla 440
Db 1411 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGACGAATCTTGACAAATGCGCC 1470
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 TACTCGCTGACCTCCAGGGCTGGGCATCAGTGGCTGGGGCTGGGCTCACTGAGGAA 1530
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1531 CTGGGCGAGTGGAGTGGCTCATCCACATAACACCCACTCTGCTGCTGCTGCAACAGGTG 1590
Qy 481 ProTrpAspGlnLeuPheAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1591 CCTGGGACCAAGCTCTTTTGGAAACCGCACCAAGCTCTGCTCCACACTGCTCCAAACCCGCA 1650
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

Db	1651		GAGGACAGGTCGTGGCGGAGGGCCTTGCCCTGCACCACGCTGTGGCCCGAGGGCACTGC	1710
Qy	521		TriGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1711		TGGGGTCACGGGCCCAACCCAGTGTGTCACTGCACGCCAGTTCCTTCGGGGCCAGGAGTGC	1770
Qy	541		ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	1771		GTGGAGGAATGCCCAGTACTGCAGGGCTCCCCAGGAGTAGTGTGAATGCCAGGCACTGT	1830
Qy	561		LeuProCysHisProGluCysGlnProGluAsnGlySerValThrCysPheGlyProGlu	580
Db	1831		TTGCCGTGCACCCCTGAGTGTACGCCCCAGAAAGCTCAGTAGCCTGTTTGACCCGGAG	1890
Qy	581		AlaAspGlnCysValAlaCysAlaHisTyrIlysAspProProPheCysValaIaArgCys	600
Db	1991		GCTGCACAGTGTGGGCTGTGCCCCACTATAAGGACCCTCCCTTCTCGGTGGCCCGCTGC	1950
Qy	601		ProSerGlyValIlysProAspLeuSerTyrMetProIleTrrIlysPheProAspGluGlu	620
Db	1951		CCCAAGCGGTGTGAACCTGACCTCTCCTACATGCCCATCTGGAAGTTTCAGATGAGGAG	2010
Qy	621		GlyValaCysGlnProCysProIleAsnCysThrHisSerCysValaAspLeuAspAspLys	640
Db	2011		GGCGCATGCCAGCCTTGCCCATCACTGACCCACTCCTGTGTGGACCTGGATGACAG	2070
Qy	641		GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	2071		GGCTGCCCCCGGAGCAGAGAGCCAGCCCTCTGACGTCCTCATCAAGCGACGGCAGCAG	2130
Qy	653	----	----	653
Db	2131		ATTCTGCTGTCGTGGTCTTTGGGGTGGTCTTTTGGATCTCTTCATCAAGCGACGGCAGCAG	2190
Qy	653	----	----	653
Db	2191		AAGATCCGAAGTACACGATCCGGAGACTGCTGCAGGAAACGGAGCTGTTGGAGCCGCTG	2250
Qy	653	----	----	653
Db	2251		ACACTAGCGGAGCGATGCCCAACAGGCGCGAGATGGGATCTCTGAAAGAGCAGCGAGCTG	2310
Qy	653	----	----	653
Db	2311		AGGAAGTGGAAGTGCTTGGATCTGGCGCTTTTGGCACAGTCTTCAAGGGCATCTGGATC	2370
Qy	653	----	----	653
Db	2371		CCTGATGGGGAGATGTGAAATTTCCAGTGGCCATCAAGTGTGTGAGGGGAAAACACATCC	2430
Qy	653	----	----	653
Db	2431		CCCAAGCCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA	2490
Qy	653	----	----	653
Db	2491		TATGTCTCCGCTTCTGGGCACTGCTGCATCATCCAGGTGACGTGTGTGACACAGCTTT	2550
Qy	653	----	----	653
Db	2551		ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAACCGCGACGCTGGGCTCCAG	2610
Qy	653	----	----	653
Db	2611		GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGCTACTGAGAGATGTGCGG	2670
Qy	653	----	----	653
Db	2671		CTCGTACACAGGAGACTTGGCGCTCGGAAAGTGTGTGTCGAAGAGTCCCAACCATGTCAA	2730
Qy	653	----	----	653

Db	2731	ATTACAGACTTCGGGCTGGCTCGCTGCTGGACATTCGACGAGACAGAGTACCATGTCAGAT	2790
Qy	653	-----	653
Db	2791	GGGGCAAGGTGCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTCACC	2850
Qy	653	-----	653
Db	2851	CACCAGAGTGATGTGTGGAGTTATGTGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2910
Qy	653	-----	653
Db	2911	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG	2970
Qy	653	-----	653
Db	2971	CTGCCCCAGCCCCCATCTGCAACCATGTGATCTACATGATCATGTGTCAAATGTTGGATG	3030
Qy	653	-----	653
Db	3031	ATTGACTCTGAATTCGGCCACGANTTCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	3090
Qy	654	-----GlnAspLeuAspLeuGlyProAlaSerProLeu	664
Db	3091	AGGAGCCCCCAGCGCTTTTGGTCAATCCAGAAATGAGACTTTGGGCCCGAGCGATCCCTTG	3150
Qy	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3151	GACAGCACCTTCTACCGCTCACTCTGTGGAGACGATGACATGGGGACCTGGTGGATGCT	3210
Qy	685	GluGlyTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly	704
Db	3211	GAGGAGTATCTGTTACCCAGCAGGCGCTTCTTCTGTCAGACCTGCGCCGGCGCTGGG	3270
Qy	705	GlyMetValHisArgHisArgSerSerSerThrArgSerGlyGlyAspLeuThr	724
Db	3271	GGCATGTGTCCACACAGGCCACCCAGCTCATCTACCAGGAGTGGCGGTGGGACCTGACA	3330
Qy	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3331	CTAGGGCTGAGGCCCTCTGAAAGAGGAGGCCCCACAGGTCTCACTGGCACCTTCGAAGGG	3390
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaIysGlyLeuGlnSer	764
Db	3391	GCTGGCTCCGATGATTTATGTGTGACCTGGGAATGGGGCAGCCCAAGGGGTGCAAAAGC	3450
Qy	765	LeuProThrHisAspProSerProLeuGlnAlaTyrSerGluAspProThrValProLeu	784
Db	3451	CTCCCCACATGACCCCGACCTCTACAGCGGTGACAGTGAGAGCCCAAGTACCCCTG	3510
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3511	CCCTCTGAGACTGATGGCTACGTTGCCCTTGCCTGACCTGCAAGCCCCCAGCTGAATGTG	3570
Qy	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3571	AAACAGCCAGATGTTGGGCCCCAGCCCTTTCGCCCCGAGAGGGGCCCTCTGCTGTGCTGCC	3630
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyIysAsnGlyVal	844
Db	3631	CGACTCTGCTGGTGCCACTCTGGAAGAGGGCCCAAGACTCTCTCCCCAGGGGAAGATGGGTC	3690
Qy	845	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3691	GTCAAAGACGTTTTTTCCTTTGGGGTGCAGTGGAGNAACCCCGAGTACTTTGACACCCCG	3750
Qy	865	GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3751	GGAGGAGTCCCTCCAGCCCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3810
Qy	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3811	TATTACTGGGACAGAGCCACAGAGCGGGGGCTCCACCCAGCACTTCAAGGGACA	3870

Qy 905 ProThrAlaGluAenProGluTyrLeuGlyLeuAspValProVal 919
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|
|
Db 3871 CCTACGGCAGAGAACCCAGAGTACCTGGTCTGGACGTCGCCAGTG 3915

RESULT 12

US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 0 Length: 9274
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
Db: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-1 (1-9274)

Qy 1 MetGluLeuAlaLeuAalaLeuCysArgTyrGlyLeuLeuAlaLeuLeuProGlyAla 20
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|
Db 1731 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCTCTTGGCCCCGGAGCC 1790
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|
|
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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|
|
Db 1791 GCGAGCACCAGTGTGCACCGGCACAGACATGAGCTGCGGCTCCCTGCGAGTCCCGAG 1850
|
|
|
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAenLeu 60
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|
|
Db 1851 ACCCACTGGACATGCTCCGCCACCTCTACCGAGGCTGCCAGTGTGCGAGGAAACCTG 1910
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|
|
Qy 61 GluLeuThrTyrLeuProThrAenAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
|
|
|
Db 1911 GAACCTCACTACTGCGCCACCAATGCGAGCTGCTCTCTCGAGGATATCCAGAGGTG 1970
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|
|
Qy 81 GlnGlyTyrValLeuIleAlaHisAenGlnValArgGlnValProLeuGlnArgLeuArg 100
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|
|
Db 1971 CAGGGCTACGCTCATCGCTCACACCAAGTGGAGCGAGTCCCACTGCGAGGCTGCGG 2030
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|
|
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAenTyrAlaLeuAlaValLeuAspAenGly 120
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|
|
Db 2031 ATTGTGCGAGGCGACCCAGCTCTTTGAGGACACTATGCTCCCTGGCCGTGTAGCAATGGA 2090
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|
|
Qy 121 AspProLeuAenAenThrThrProValThrGlyValaSerProGlyGlyLeuArgGluLeu 140
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|
|
Db 2091 GACCCGCTGACATATACACCTCTGCACAGGGGCTCCCGCAGAGGCTTGGCGAGCTG 2150
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|
|
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAenProGln 160
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|
|
Db 2151 CAGCTTCGAAGCTCACAGAGATCTTGAAAGAGGGGTCTTGATCCAGCGGAAACCCCGAG 2210
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|
|
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAenAenGlnLeuAla 180
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|
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Db 2211 CTCGTCTACGAGCACGATTTTGTGGAAGGACATCTTCCACAGAACCAACCAGCTGGCT 2270
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|
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Qy 181 LeuThrLeuIleAspThrAenArgSerArgAlaCysHisProCysSerProMetCysLys 200
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|
|
Db 2271 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCCCCTGTCTCTCCGATGTGTAAAG 2330
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|
Qy 201 GlySerArgCysTyrGlyLeuSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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|
|
Db 2331 GGCTCCCGCTCTCGGGAGAGATTCTGAGGATTGTGAGGCTGACGGGCACTGTCTCT 2390
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|
|
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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|
Db 2391 GCGGTGGCTGTGCCCGCTGCAGGGGCCACTTGCCTGCTGCTGCTGCTGCTGCTGCTGCT 2450
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Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAenHis 260
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|
Db 2451 GCTGCCGCTGCAACGGGCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCT 2510
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Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAenThrAspThrPheGlu 280
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|
Db 2511 AGTGCATCTGTGAGCTGACTTGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2570
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Qy 281 SerMetProAenProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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|
Db 2571 TCCATGCCCAATCCCGAGGGCGGTATACATTTGGCGGCGAGCTGTGTGACTGCTGCT 2630
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|
|
Qy 301 TyrAenTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAenGln 320
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|
Db 2631 TACAACTACCTTTCTACGAGCGTGGGATCTGTCACCTGCTGCTGCTGCTGCTGCTGCT 2690
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Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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Db 2691 GAGGTGACAGCAGAGAGATGGAAACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCGA 2750
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Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAen 360
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|
Db 2751 GTGTCTATGTCTGCGCATGGGACATTTGCGAGAGGTGAGGCGAGTTACCACTGCTGCT 2810
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|
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerIleuAlaPheIleuProGluSer 380
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|
|
Db 2811 ATCCAGGAGTTTGTCTGGCTGCAAGAGATCTTTTGGAGGCTTGGCATTTCTGCCGGAGAGC 2870
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|
Qy 381 PheAspGlyAspProAlaSerAenThrAlaProLeuGlnProGluGlnValPhe 400
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|
Db 2871 TTTGATGGGACCCAGCCCTCCAACTGCTGCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 2930
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|
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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Db 2931 GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGGCGCGAGCCCTG 2990
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Qy 421 AspLeuSerValPheGlnAenLeuGlnValIleArgGlyArgIleLeuHisAenGlyVala 440
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|
Db 2991 GACCTCAGCGTCTTCAGAACTTGCAGTAATTCGGGGAGCAATTTCTGCACATGGCGCC 3050
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Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
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Db 3051 TACTCGTCACTGCTGCAAGGCTTGGCATCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3110
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Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAenThrHisLeuCysPheValHisThrVal 480
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Db 3111 CTGGGCGATGGAGTGGCTCTCATCCACCATTAACACCCACTCTGCTGCTGCTGCTGCTGCT 3170
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|
Qy 481 ProTyrAspGlnLeuPheArgAenProHisGlnAlaLeuLeuHisThrAlaAenArgPro 500
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Db 3171 CCTTGGGACAGCTCTTTTCGAAACCCGACCAAGCTTCTGCTCCACACTGCTCCACCGGCCA 3230
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|
Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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Db 3231 GAGACAGAGTGTGTGGCGGAGGCTTGGCTGCTGCCACCACTGCTGCTGCTGCTGCTGCT 3290
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Qy 521 TrpGlyProGlyProThrGlnCysValAenCysSerGlnPheLeuArgGlyGlnGluCys 540
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Db 3291 TGGGGTCCAGGGGCCCACTGCTGTCACTGAGGCGAGTCTCTTCTGCGGGCGGAGGTGC 3350
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QY 541 ValGluGluCysArgValLeuGlnGlyLeuProAArgGluPyrValAsnAlaArgHisCys 560
Db 3351 GTGGAGGAATGCCAGTACTGCAAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 3410
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 3411 TTGCCGTGCCACCTCGAGTGTACGCCCAAGAAATGGCTCAGTGACCTGTGTTTGGACCGGAG 3470
QY 581 AlaAspGlnCysValAlaCysAlaHisIstYrLysAspProPheCysValAlaArgCys 600
Db 3471 GCTGACCAAGTGTGGCTGTGCCCACTATAGGACCTCCCTCTCTGCGTGGCCCGCTGC 3530
QY 601 ProSerGlyValLysProAspLeuSerPyrMetProIlePrlLysPheProAspGluGlu 620
Db 3531 CCACGGGTGTGAACCTGACCTCTCTACATGCCATCTGGAAGTTCAGATGAGGAG 3590
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspPyls 640
Db 3591 GGCGCATGCCAGCTTTGCCCATCAATGACCACTCTCTGTGTGTGACCTGGATGACAAG 3650
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 3651 GCTGCCCCCGGAGCAGAGAGCCAGCCCTCTGACCTCCATCTCTGCGGTGTGGC 3710
QY 653 653
Db 3711 ATTCTGCTGCTGCTGTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG 3770
QY 653 653
Db 3771 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCAGGAAACGGAGCTGTGGAGCCGCTG 3830
QY 653 653
Db 3831 ACACCTAGCGGAGCGATGCCAACACAGCGGCAGATGGGATCCTGAAAGAGACGGAGCTG 3890
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Db 3891 AGGAAGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTCAAGGGGCATCTGGATC 3950
QY 653 653
Db 3951 CCTGATGGGGAGAAATGTGAAATTCAGTGGCCATCAAAAGTGTGTGAGGGAACACATCC 4010
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Db 4011 CCCAAGGCCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA 4070
QY 653 653
Db 4071 TATGTCTCCCGCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGTGTGACACAGCTT 4130
QY 653 653
Db 4131 ATGCCCTATGGCTGCTCTTAGACCATGTTCGGGAAACCGCGGACGCTGTGGGCTCCGAG 4190
QY 653 653
Db 4191 GACCTGCTGAACTGGTGTATGACAGATTTGCCAAGGGGATGAGCTACTGGAGGATGTGGG 4250
QY 653 653
Db 4251 CTGCTACACAGGACTTGGCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 4310
QY 653 653
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Db 4551 CTGCCCCAGCCCCCATCTGCAACATTTGATGTCTACATGATCATGGTCAAAATGTTGGATG 4610
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QY 685 704
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US-08-229-515A-14
: Sequence 14, Application US/08229515A
: Patent No. 5518885
: GENERAL INFORMATION:
: APPLICANT: RAZIUDIN
: APPLICANT: SARKAR, FAZLUL H
: TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
: TITLE OF INVENTION: NEOPLASTIC DISEASE
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NEEDLE & ROSENBERG PC
: STREET: 127 Peachtree Street, Suite 1200
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/229,515A
: FILING DATE: 19 APR 1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: PERRYMAN, DAVID G
: REGISTRATION NUMBER: 33,438
: REFERENCE/DOCKET NUMBER: 1414.608
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 404-688-9880
: TELEFAX: 404-688-9880
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3955 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-229-515A-14

Alignment Scores:
Pred. No.: 6,238-298 Length: 3955
Score: 4134.00 Matches: 781
Percent Similarity: 65.47% Conservative: 42
Best Local Similarity: 62.13% Mismatches: 96
Query Match: 81.41% Indels: 338
DB: 1 Gaps: 3

US-09-493-480-6 (1-919) x US-08-229-515A-14 (1-3955)

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Qy	61	GluLeuThrTyrrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspGlnGluVal	80
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Db	266	CAGGGTTACATCTCATCTGTACCAACCAAGGAGCGCGCTCCCACTGTCAAGAGCTGCG	325
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspGln	120
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Qy	121	AspProLeuAsnAsnThrThrProValThr---GlyAlaSerProGlyGlyLeuArgGlu	139
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Qy	160	GlnLeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeu	179
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 13:54:19 ; Search time 830.537 Seconds

(without alignments)
5047.907 Million cell updates/sec

Title: US-09-493-480-6

Perfect score: 5078

Sequence: 1 MELAALCRWGLLALLPGA.....TFKGTPTAENPEYLGLDVPV 919

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4900	96.5	3768	9	US-09-930-125-1	Sequence 1, Appli
3	4900	96.5	3768	13	US-09-765-973-1	Sequence 1, Appli
4	4900	96.5	3768	15	US-10-313-644-1	Sequence 5, Appli
5	4900	96.5	4473	10	US-09-441-411-5	Sequence 32, Appli
6	4900	96.5	4473	15	US-10-146-473-32	Sequence 44, Appli
7	4900	96.5	4473	15	US-10-207-655-44	Sequence 81, Appli
8	4900	96.5	4473	15	US-10-101-510-81	Sequence 5, Appli
9	4892	96.3	3768	9	US-09-811-123-8	Sequence 8, Appli
10	4892	96.3	3768	9	US-09-811-115-2	Sequence 2, Appli
11	4892	96.3	3768	13	US-09-984-092-3	Sequence 3, Appli
12	4892	96.3	3768	13	US-10-280-576-3	Sequence 3, Appli
13	4892	96.3	4530	9	US-09-877-177-11	Sequence 11, Appli
14	4892	96.3	4530	13	US-10-392-113-45	Sequence 45, Appli
15	4892	96.3	4530	13	US-10-426-836-11	Sequence 11, Appli
16	4892	96.3	4530	15	US-10-177-293-125	Sequence 125, App
17	4892	96.3	4530	15	US-10-007-926A-119	Sequence 119, App
18	4892	96.3	4530	15	US-10-338-730-1	Sequence 1, Appli
19	4892	96.3	4530	15	US-10-101-510-124	Sequence 124, App
20	4892	96.3	4530	16	US-10-116-275-131	Sequence 131, App
21	4892	96.3	4530	16	US-10-272-437A-27	Sequence 27, Appli
22	4892	96.3	4530	16	US-10-117-937-595	Sequence 595, App
23	4892	96.3	4530	16	US-10-159-563-208	Sequence 208, App
24	4892	96.3	4530	16	US-10-435-696-10	Sequence 10, Appli
25	4892	96.3	4530	16	US-10-198-846-10896	Sequence 10896, A
26	4892	96.3	4530	9	US-09-811-123-7	Sequence 7, Appli
27	4892	96.3	9274	9	US-09-811-115-1	Sequence 1, Appli
28	4892	96.3	9274	9	US-09-971-392-70	Sequence 70, Appli
29	4880	96.1	4606	10	US-09-769-508-1	Sequence 1, Appli
30	4849	95.5	4543	9	US-09-870-759-117	Sequence 117, App
31	4134	81.4	3955	9	US-09-854-356-10	Sequence 10, Appli
32	4134	81.4	3955	10	US-09-751-708A-117	Sequence 117, App
33	4134	81.4	3955	10	US-09-854-356-11	Sequence 11, Appli
34	4125.5	70.9	2164	16	US-10-412-804A-5	Sequence 5, Appli
35	3598.5	70.9	2164	16	US-10-412-804A-9	Sequence 9, Appli
36	3595	70.8	2149	16	US-10-412-804A-3	Sequence 3, Appli
37	3521	69.3	2132	16	US-09-821-883-8	Sequence 8, Appli
38	2585	50.9	1692	9	US-09-821-883-9	Sequence 9, Appli
39	2585	50.9	2091	9	US-09-821-883-6	Sequence 6, Appli
40	2573.5	50.7	1665	9	US-09-821-883-7	Sequence 7, Appli
41	2573.5	50.7	2070	9	US-10-412-804A-1	Sequence 1, Appli
42	2497.5	49.2	1479	16	US-09-725-433-1	Sequence 75, Appli
43	1645	32.4	3633	9	US-10-236-417-75	Sequence 1, Appli
44	1645	32.4	3633	13	US-10-387-252-1	Sequence 1, Appli
45	1645	32.4	5532	13		

ALIGNMENTS

RESULT 1

US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens

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Db 1801 CCCAGCGGTGTGAACCTGACCTCTCTTACATGACCTCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GGCGCATGCCAGCTTGGCCCATCACTGCACTCCCTCTGTGTGGACCTGGATGACAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCGCGAGCAGAGGCCCTCTGAGTCCATCTCTGCGGTGGTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCGTGTGTGGTCTTGGGGGTGTCTTGGGATCTCTCATCAAGCGACGCGCAG 2040
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Db 2041 AAGATCCGGAGTATACGATCGGAGACTGTCTGCGAGAAACGGAGCTGTGGAGCCCGCTG 2100
Qy 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCCAACCGCGCGCAGATGCGGATCTCTGAAGAGACGGAGCTG 2160
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Db 2161 AGGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCCACAGTCTACAAAGGCGATCTGGATC 2220
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Db 2221 CCTGATGGGAGAGATGTGAATAATTCAGTGGGCCATCAAAAGTTGTGAGGGAAAAACATCC 2280
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Db 2461 GACTGTCTGAATGTGTATGACAGATTGCCNAGGGGATGAGCTACTGGAGGATGTGGG 2520
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Db 2581 ATTACAGACTTCCGGCTGGCTCGCTGTGTGATGATGATGAGATTCACGAGACAGAGTACCATG 2640
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Db 2701 CACAGAGTGTATGTGGAGTTATGTGTGATGTGTGGAGCTGATGATCTTTTGGGGCC 2760
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Db 2821 CTGCCCCAGCCCCCATCTGACACCATGTGATGTCTACATGATCATGTCAATGTTGGATG 2880
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Db 2881 ATTGACTCTGAATGTTCGCCAAGATTTCGGGAGTTGGTGTCTGAAATTTCTCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGACCCAGCGCTTGTGGTCTATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCTCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTCTACCGCTCACTGTGGAGGACGATGATCATGCGGGACCTGTGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGATATCTGTGTACCCAGCAGCGCTTCTCTGTCCAGACCTCTGCCCGCGCTGG 3120
Qy 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyValAspLeuThr 724
Db 3121 GGCATGGTCCACCAAGGACCGCAGCTCATCTACAGAGTGGCGGTGGGACCTTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCGCCAGCTCTCCACTGSCACCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGTGTGACCTTGGGAATGGGGGACGCAAGGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGCTAGCTTGGCCCCCTGACCTGCGAGCCCCAGCTGAAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProSerProArgGluGluGlyProLeuProAlaAla 824
Db 3421 AACGAGCGAGATGTTGGCCCCCGCCCTTGGCCCCGAGAGGGGCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACTGCTGTGTGCACCTCTGGAAGGCCCAAGACTCTCTCCCCAGGGAGAAATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGAGTCTTTCCTTGGGGTGCCTGGAGAACCCCGAGTACTTGACACCCAC 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCTCCCTCAGCCCCACCTCTCTCTGCTTTCAGCCCCAGCTTTCACACCTC 3660
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCAAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAGGGACA 3720
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Db 3721 CCTACGCGAGAGAACCCAGAGTACTCTGGGTCTGGACGTGCCAGTG 3765

RESULT 2

US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.

Qy	601	ProSerGlyVallysProAspLeuSerTyrMetProIletrIylsPheProAspGluGlu	620
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Qy	621	CCAGCGGTGTGAAACCTTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	1860
Db	1861		
Qy	641	GlyAlaCysGlnProCysProlIleAsnCysThrHisSerCysValIleAspLeuAspLys	640
Db	1861	GGGCGATGCCAGGCTTGGCCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG	1920
Qy	641		
Db	1921	GlyCysProAlaGluGlnAlaGlaSerProLeuThrSer	653
Qy	653	GGTGCCCCCGGAGCAGAGACGAGCCCTCTGACGTCATCATCTCTCGCGTGGTGGC	1980
Qy	653	-----	
Db	1981	ATTCTGCTGCTGTGGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2040
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Db	2041	AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAAACGGAGCTGTGTGGAGCGGCTG	2100
Qy	653	-----	
Db	2101	ACACCTAGCGGAGCGATGCCCAAACGAGCGCAGATCGGATCTCTGAAGAGACGGAGCTG	2160
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Db	2161	AGGAGGTGAAGGTCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGCGATCTCGATC	2220
Qy	653	-----	
Db	2221	CCTGATGGGGAGAATGTGAAATTTCCAGTGGCCATCAAGTGTGTGAGGGAAACACATCC	2280
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Db	2281	CCCAAGCCCAACAAAGAAATCTTAGACGAAGCATATCGTGTGCTGTGTGGCTTCCCA	2340
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Db	2341	TATGTCTCCGCTTCTGGGGATCTGGCTGACATCCAGGTGCAGCTGTGTGACACAGCTT	2400
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Db	2401	ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGGACGCTGGGCTCCAG	2460
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Db	2461	GACCTGTGAACCTGGTGTATCGAGTTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG	2520
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Db	2521	CTCGTACACAGGGACCTTGGCGGCTCGGAAACGTGCTGTGTCAAGATGCCAACCATGTGAAA	2580
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Db	2581	ATTACAGACTTTCGGGCTGGCTGCGCTGCTGGAACATTGACGAGACAGAGTACCATGCGAGAT	2640
Qy	653	-----	
Db	2641	GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGAGTCCATTTCTCGCGCGGCGGTTCCAC	2700
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Db	2701	CACAGAGTGAATGTGTGGAGTTATGGTGTGACTGTGTGTGGAGCTGATGACTTTTGGGGCC	2760
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Db	2761	AAACCTTACGATGGGATCCCHAGCCGGGAGATCCCTGACCTGTGGGAAAGGGGAGCGG	2820
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Db	2821	CTGCCCGAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGGATG	2880

QY	653	-----653	
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QY	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
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QY	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
DB	3001	GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT	3060
QY	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
DB	3061	GAGGAGTATCTGGTATCCCAAGCAGCGGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGGG	3120
QY	705	GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyGlyAspLeuThr	724
DB	3121	GGCATGTGTCCACACAGCGACCGAGCTCATCTACAGGAGTGCGCGGTGGGACCTGAC	3180
QY	725	LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly	744
DB	3181	CTAGGGCTGAGCGCTCTGAGAGGAGGCCCCACAGGTCTCCACTGGCCACCTCCGAAGG	3240
QY	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaIysGlyLeuGlnSer	764
DB	3241	GCTGGCTCCGATGTAATTGATGTGTGACCTGGGAATGGGGGAGCAAGGGGCTGCAAGC	3300
QY	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
DB	3301	CTCCCCACACATGACCCACCGCTCTACAGCGGTACAGTGGAGACCCCAAGATACCCCTG	3360
QY	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
DB	3361	CCCTCTGAGACTGATGCTAGCTTGGCCCCCTGACCTGAGCCGCCAGCTGAATATGTG	3420
QY	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
DB	3421	AAACAGCCAGATGTTTGGCCCCCAGCCCTTGGCCCCGAGAGGAGCCCTCTGCTGCTGCC	3480
QY	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyIlysAsnGlyVal	844
DB	3481	CGACTCTCTGGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGAAGAATGGGGTC	3540
QY	845	ValIysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
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QY	865	GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu	884
DB	3601	GGAGGAGCTGCCCTCAGCCGCCACCCCTCTCTCTCTCTTCCAGCCAGCTTTCGACACCTC	3660
QY	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheIysGlyThr	904
DB	3661	TATTACTGGGACCAAGACCCACAGAGCGGGGGGCTCCACCCAGACTCTTCAAGGGGAC	3720
QY	905	ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
DB	3721	CCTACGGCAGAGAACCCAGAGTACTTGGGTCTGGACGTGCGAGTG	3765
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; Sequence 1, Application US/09765973			
; Publication No. US20020039573A1			
; GENERAL INFORMATION:			
; APPLICANT: Cheever, Martin A.			
; APPLICANT: Hand-Zimmermann, Susan			
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND			
; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES			
; FILE REFERENCE: 210121.496			
; CURRENT APPLICATION NUMBER: US/09/765,973			
; CURRENT FILING DATE: 2001-01-19			
; NUMBER OF SEQ ID NOS: 4			

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 3768

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1) ... (3765)

US-09-765-973-1

Alignment Scores:

Pred. No.: 0 Length: 3768

Score: 4900.00 Matches: 919

Percent Similarity: 73.23% Conservative: 0

Best Local Similarity: 73.23% Mismatches: 0

Query Match: 96.49% Indels: 336

DB: 13 Gaps: 1

US-09-493-480-6 (1-919) x US-09-765-973-1 (1-3768)

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DB 61 GCGAGCACCAAGTGTGACCGGACAGACATGAAGCTGCGCTCCCTGCGAGTCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
DB 121 ACCACCTGGACATGCTCGGCCACTTACAGGGCTGCCAGGTGTGTGAGGAAACCTG 180
QY 61 GluLeuThrTyrrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 181 GAACCTACCTACTGCTGCCACCAATGACAGCTGTCTTCTGCGAGTATCCAGGAGTG 240
QY 81 GlnGlyTyrrValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 241 CAGGGCTAGCTGCTCATCGCTCAACACCAAGTGGAGGCTGCCACTGCGAGAGCTGCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspAsnGly 120
DB 301 ATTGTGCGAGGACCAAGCTCTTTGAGGACACTATGCGCTTGGCGGTGTGTAGCAATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 361 GACCCGCTGAACATACCAACCCCTGTACAGGGGCTCCCGAGAGGCTGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
DB 421 CAGCTTCGAAGCCTCAAGAGATCTTGAAGGAGGGGTCTTTGATCCAGCGGAAACCCCGCAG 480
QY 161 LeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 481 CTCTGCTACAGGACAGATTTGTGAAGGACATCTTCCACAGAAACACCAAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 541 CTACACTGATAGACCAACACCGCTCTCGGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG 600
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 601 GGCCTCCGCTGCTGGGAGAGATTTCTGAGGATTTGTGAGAGCTTCAGAGCCTGAGCGCTGT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 661 GCCGGTGGCTGTGCGGCTGCAAGGGGCGCACTGCGCCACTGACTGCTGCCATGAGCAGTGT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCCGGCTGACAGGGGCCCCAGCACTCTGACTGCTGCGCTGCCCTCCACTTCAACAC 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrrAsnThrAspThrPheGlu 280
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DB 841 TCCATGCCCAATCCCGAGGCGCGGTATACATTGGCGCGCAGCTGTGTGACTGCTGTCTCC 900
QY 301 TyrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACCTACTCTTCTACGGACGTGGGATCTGACACCTCTGCTGCGCCCTGCAACACCA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAAGTGCAGCAGCCCTGTGCCCGGA 1020
QY 341 ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGCTTGGGCTGAGGACATTCGAGAGGTGAGGGCAGTTACCAAGTCCCAAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGGAGTTTGTCTGGCTGCAAGAAAGATCTTTGGGAGCCTGGCATTTCTGCCGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1141 TTTGATGGGAGCCAGCCTCCAACTGCCCCCTCCAGCCAGCAGCAGCTTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrrLeuTyrrIleSerAlaTrpProAspSerLeuPro 420
DB 1201 GAGACTCTGGAAGAGATCACAGGTACCTATATATCTCAGCATGCCCGGACAGCTGCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGCTCTTCAGAACTGCAAGTAATCCGGGAGCAATTTCTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCTACTGAGGGA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGAGTGGCCCTCATCCACATAACACCCACCTCTGCTGCTGTCACACGCTG 1440
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGGAGCAGCTCTTTCGAAACCCCGACACAGCTCTGTCTCCACACTGCCAACCGGCA 1500
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGCGGAGGGCTGGCTGCCACCAAGCTGTGCGGCCGAGGAGTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGCTCCAGGGCCCACTGCTGCTCACTGAGCAGCTGCTTCTGGGGCGCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATGCGGAGTACTGCGAGGGCTCCCGAGGAGTATGTGAATGCCAGGACACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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DB 1741 GCTGACCAAGTGTGGCTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrrMetProIleTrpLysPheProAspGluGlu 620
DB 1801 CCCAGCGGTGAAACCTGACCTCTCTATACATGCCCATCTGGAAGTTCCTCAGATGAGGAG 1860
QY 621 GlyValaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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Db 1861 GGCGCATGCCAGCTTGGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 1920
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Db 1921 GGCTGCCCGCCGAGCAGAGAGAGCCAGCCCTCTGACGTCCATCATCTCGCGGTGGTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCTGCTGCTGTGTCTTGGGGGTGGTCTTTGGGATCTCTCATCAAGCGACCGCAGCAG 2040
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Db 2041 AAGATCCGGAAGTACACGATGCGGAGACTCTGTCAGGAACCGGAGCTGTGGAGCCGCTG 2100
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Db 2101 ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGCGGATCTCTGAAAGAGACGGAGCTG 2160
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Db 2161 AGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
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Db 2221 CCTGATGGGGAATGTGAAATTCAGTGGCCATCAAGTGTGTGGGAAACACATCC 2280
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Db 2461 GACCTGCTGAATGGTGTATGCAGATTGCCAAGGATGAGTACCTGGAGGATGTGCGG 2520
Qy 653 ----- 653
Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGTCAAGAGTCCAAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTGGGCTGGCTGGCTGCTGGAATTGACGAGACAGATACCATGCAGAT 2640
Qy 653 ----- 653
Db 2641 GGGGGCAAGGTGCCATCAAGTGAATGGCGCTGGAGTCCATTTCTCCGCGGCGGTTCACC 2700
Qy 653 ----- 653
Db 2701 CACCAGATGATGTGTGAGATTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCCGAGCCGGGAGATCCCTGACCTGTGGAAGGGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAAATGTTGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTGTGTGTCTGTAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGACCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGCCCGCAGCTCCCTTG 3000
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Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTTACCCGCTCACTCTGTGAGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGAGATATCTGTGTACCCGACGAGGCTTCTTGTTCAGACCCCTGCCCCCGGCGCTGG 3120
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACACACAGCCAGCTCATCTACAGGAGTGGCGTGGGACCTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGAGGCGCCCTTCTCACTGGCACCTTCCGAAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGTATTTGATGTGACTGGGATGGGGGAGCCAGGGGCTGCAGAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACATGACCCCGCCCTTACAGCGGTACAGTGGAGGACCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGTGTGCTTGGCCCTTACCTGACGCCCCCAGCCTTGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCGCCAGATGTTGGCCCCCAGCCCCCTTGGCCCCGAGAGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTCCACTCTCTGGAAGGCCCAAGACTCTCTCCCCAGGAGAAAGTGGGTC 3540
Qy 845 ValIysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGACGCTTTTGTGCTTGGGGGTGCCGTGGAGAACCCCGAGTACTTGACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCTGAGCCCCACCTCTCTCTGCTTCCAGCCAGCCTTTCAGAACCTC 3660
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCAAGGACCCACAGAGCGGGGGCTCCACCAGCACCTTCAAGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACTTGGGTCTGGACGTCGCCAGTG 3765
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RESULT 4

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US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)....(3765)
US-10-313-644-1

Alignment Scores:

Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-6 (1-919) x US-10-313-644-1 (1-3768)

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Db 1 ATGGAGCTGGGGCTTGTGGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCCGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCCCAAGTGTGCACCGGCCACAGACATGAAGCTGGCGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTrpGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACCTGGACATCTCCGCCACTCTTACAGAGGCTGCCAGTGGTGCAGGGAACCTG 180
Qy 61 GluLeuThrTrpLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 181 GAACCTCACTACCTGCCCAACCAATGCCAGCCTGTCTCTCTGCAGATATCCAGGAGTG 240
Qy 81 GlnGlyTrpValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGTGTCTATCTGCACCAACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGGCG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTrpAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCCACCGAGCTCTTTGAGGACACTATATGCCCTGGCGTGTGTAGCAATGA 360
Qy 121 AspProLeuAsnAsnThrTrpValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAAATACCAACCCCTGTGCAGGGGGCTCCCGAGGAGGCTGGCGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 480
Qy 161 LeuCysTrpGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACCGAGACACGATTTTGTGAAGGACACTTTCACAGACACACACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACATGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAAG 600
Qy 201 GlySerArgCysTrpGlyLysSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCCTCCGCTGTGGGGAGAGTCTTGAGGATTTGCAGGCTTCAGCGGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys 240
Db 661 GCGGGTGGTGTGGCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCAOGGGCCCCAAGCACTCTGACTGCTGGCTGGCTGCCCTTCAACCCAC 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACTGCCCGCCCTGGTCACTTACCAACACAGACAGCTTGAG 840
Qy 281 SerMetProAsnProGluGlyArgTrpThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCCCAATCCCGAGGGCCGGTATATCATTTGGGGCCAGCTGTGTGACTGCTGCC 900
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Qy 301 TyrAsnTrpLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACCTACCTTTCTACGGACGTGGATCTCTGACCCCTGCTGCCCCCTTGCACAACCAA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACAGCAGAGAGTGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCCA 1020
Qy 341 ValCysTrpGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGCGAGTTCACAGTGCCAAT 1080
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGTGTGTGCTGCTGCAAGAGATCTTTGGAGGCTTGCAATTTCTGCCGAGAGC 1140
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGACCCAGCCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCAAAGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTrpLeuTrpIleSerAlaTrpProAspSerLeuPro 420
Db 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATATCATCTCAGCATGGCGGACAGCTGCCT 1260
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1261 GACCTCAGCGCTTCCAGAACCTGCAAGTAATCCGGGGAGCAATTTCTGCAATGGCGCC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTGAGGAA 1380
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGCGAGTGAGCTGGCCCTCATCCACCAATAACACCTCTCTGCTCTGCTGCACAGTG 1440
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1441 CCTTGGGACCACTCTTTCGGAACCCGACCAAGCTCTGCTCCTCACTGCAACCCGCCA 1500
Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGTGGCGAGGGCTGGCTGCCACCACTGTGCTGCCAGGAGGCACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGGTCCAGGGGCCACCCAGTGTGTCAACTGCAGCCAGTTCTTCCGGGCCAGGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrpValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCAGTACTTGCAGGGGCTCCCGAGGAGTATGTGATGTCAGGCACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTTCCGCTGCCACCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTrpLysAspProPheCysValAlaArgCys 600
Db 1741 GCTGACAGTGTGGCCCTGTGCCACTATAGGACCTCCCTCTTCTGCGGGCCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTrpMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAGTTCCTGAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GCGCATGCCAGCCTTTGCCCCCATCACTGACCCACTCTCTGTGTGAGCTGGATGCAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGTGCCCCCGGAGCAGAGAGCAGCCCTCTGACGTCCATCATCTCTCGGTGGTGGTGGC 1980
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Qy 653 ----- 653
Db 1981 ATTCTGCTGTCGTGCTTTGGGGTGTCTTTGGGATCTCTCATCAAGCCAGCCGACGAG 2040
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Db 2041 AAGATCCGGAGTACACGATCGGAGACTGCTGCGAAACGGAGCTGGTGGAGCCGCTG 2100
Qy 653 ----- 653
Db 2101 ACACCTAGCGAGCGATGCCCAACAGCGCGAGATGCGATCTCTGAAAGACGAGCTG 2160
Qy 653 ----- 653
Db 2161 AGGAAGTGAAGTGTCTGGATCTGGCGCTTTTGGCAAGTCTACAGGGCATCTGGATC 2220
Qy 653 ----- 653
Db 2221 CTTGATGGGAGATGTGAATAATTCAGTGGCCCATCAAGTGTGAGGGAAACACATCC 2280
Qy 653 ----- 653
Db 2281 CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGGCTGCCCA 2340
Qy 653 ----- 653
Db 2341 TATGTCTCCCGCTTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2400
Qy 653 ----- 653
Db 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGGAGCGCTGGGCTCCGAG 2460
Qy 653 ----- 653
Db 2461 GACCTGTGAACTGGTGTATCAGATTGCCAAGGGATGACTACTCTGGAGATGTGCGG 2520
Qy 653 ----- 653
Db 2521 CTCGTACACAGGAGCTTGGCGCTCGGAACTGTGCTGCTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGACATTTGACGAGACAGAGTACCATGCAGAT 2640
Qy 653 ----- 653
Db 2641 GGGGCAAGTGGCCATCAAGTGGATGGGCTGGAGTCCATTCTCCGCGCGGTTCCACC 2700
Qy 653 ----- 653
Db 2701 CACCAGATGATGTGTGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACTGCTGGAAAGGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTGGCCAAAGATTCCGGAGTTGGTGTGTAATTTCCCGCATGGCC 2940
Qy 654 ----- GlnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTCTACCGCTCTACTGCTGGAGGACGATGATGAGGAGGAGCTGGTGGATGCT 3060
Qy 685 GluGlyTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704

Db 3061 GAGGAGTATCTGGTACCCAGCAGCGCTTCTTGTTCAGACCTTCGCCCGGCGCTGG 3120
Qy 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGTTCCACACACGCGACCGAGCTCATCTACAGAGTGGCGGTGGGACCTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCTGGAGCGCTCTGAAGAGAGAGCGCCCGAGGTCTCCACTGGCACCTTCGAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGGTGGACCTGGGAATGGGGGAGCCAGAGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACACATGACCCCGCCCTCTACAGCGGTACAGTGGAGGCCCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlyTyrVal 804
Db 3361 CCCTCTGAGACTGATGGCTAGCTTGGCCCTTGGCCCTGACCTGCAGCCCCCAGCTGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCAGCGAGATTTGGGCCCTTGGCCCTTGGCCCGAGAGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACTGCTGTGCTCACTCTGGAAGGCCCAAGACTCTCTCCCGAGGGAAGTGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGACGTTTTTGGCTTTGGGGTGGCGTGGAGAAACCCGAGTACTTGCACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGAGCTGCCCTCTCAGCCCCACCTCTCTCTCTTTCAGCCCGAGCTTCGACAACTTC 3660
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACAGGACCCAGAGCGGGGGCTCCACCCAGCACCTTCAAGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAAACCCAGAGTACTCTGGGTCTGGAGCTGCCAGTG 3765

RESULT 5

US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Inggerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:

Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0

	Query Match:	96.4%	Indels:	336	
	DB:	10	Gaps:	1	
	US-09-493-480-6 (1-919) x US-09-441-411-5 (1-4473)				
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Qy	21 AlaserThrGlnValCysThrGlyThrAspMetIlysLeuArgLeuProAlaSerProGlu 40				
Dd	235 GCGAGCACCAAGGTGCACCGGCACAGCATGAAGCTGGGGCTCCCTGCGCATGCCCGGAG 294				
Qy	41 ThrHisLeuAspMetLeuArgHisLeuTyrglnclyCysGlnValValGlnGlnGlyAsnLeu 60				
Dd	295 ACCCACCTGACATGCTCCGCCACTCTACAGGGCTGCCAGGTGGTGCAGGAAACCTG 354				
Qy	61 GluLeuThrTyrlLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80				
Dd	355 GAATCACTACCTGCCACCACCAATGCCAGCTGTCTCTCTGTCGAGGATATCCAGGAGGTG 414				
Qy	81 GlnGlyTyrlValLeulleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100				
Dd	415 CAGGGCTACGTGCTCATCGCTCAACAAGTAGGAGGCTCCACCTGCAGAGGGCTGCCG 474				
Qy	101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrlAlaLeuAlaValLeuAspAsnGly 120				
Dd	475 ATTGTGGAGGACCCAGCTCTTTGAGGACNACTATGCTCTGGCGGTGTAGACATATGGA 534				
Qy	121 AspProLeuAsnAsnthrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140				
Dd	535 GACCCGCTGAACAATAACACCCCTGTTCACAGGGGCTCTCCCAGGAGGCTTGCGGAGCTG 594				
Qy	141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeulleGlnArgAsnProGln 160				
Dd	595 CAGCTTCGAGGCTTCACAGAGATCTTGAAGAGGGGTCTTGATTCAGCGGAACCCCGAG 654				
Qy	161 LeuCystyrGlnAspThrIleLeuTrpLysAspilePheHisIlysAsnAsnGlnLeuAla 180				
Dd	655 CTCTGCTACCAGGACACGATTTTGTGAAGGACATCTTCCACAAGAACAACACAGCTGGCT 714				
Qy	181 LeuThrIleuleaspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200				
Dd	715 CTCACACTGTATGACACCAACCGCTCTCGGGGCTGCCACCCCTGTCTCCGATGTGTAA 774				
Qy	201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220				
Dd	775 GGCTCCCGCTGCTGGGGAGAGATTCTGAGATTGTTCAGAGCCTGACGGCCACTGCTGT 834				
Qy	221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240				
Dd	835 GCCGGTGGCTGTGCCCTGTCAGAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894				
Qy	241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260				
Dd	895 GCTCCCGGCTGACGGGCCCCAGACACTCTGACTGCTGGCGCTGCCCTCCACTTCAACCAC 954				
Qy	261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrlAsnthrAspThrPheGlu 280				
Dd	955 AGTGGCATCTGTGAGCTGCATGCTGCCAGCCCTGGTGCACCTTACAACAACAGACAGTGTGAG 1014				
Qy	281 SerMetProAsnProGluGlyArgTyrlThrPheGlyAlaSerCysValThrAlaCysPro 300				
Dd	1015 TCCAATGCCCAATCCCGAGGGCGGTATATACATTTGGCGGCCAGCTGTGTGACTGCTGTCCC 1074				
Qy	301 TyrlAsnTyrlLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320				
Dd	1075 TACAACCTACCTTYCTACGGAGCTGGGATCTGTCAACCTGTGCTGCCCTCTGCACACCAA 1134				
Qy	321 GluValThrAlaGluAspGlyThrGlnArgCysGlnLysCysSerIlysProCysAlaArg 340				
Dd	1135 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1194				

Db 2275 ACACCTAGCGGAGCGATGCCCAACCAAGCGCAGATCGGATCTCTGAAGAGACGAGCTG 2334
QY 653 ----- 653
Db 2335 AGGAAGGTGAGGTGCTTGATCTGGGCTTTTGGCACAGCTTACAAGGGCACTGGATC 2394
QY 653 ----- 653
Db 2395 CCTGATGGGAGAATGTGAATAATTCAGTGGCCATCAAGTGTGAGGGAACACATCC 2454
QY 653 ----- 653
Db 2455 CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGCTGCTGGGCTCCCA 2514
QY 653 ----- 653
Db 2515 TATGTCTCCGCTTCTGGGCACTCTGCTGACATCCAGGTGACGTGGTGACACAGCTT 2574
QY 653 ----- 653
Db 2575 ATGCCCTATGCTGCTCTTTAGACCAATGTCGGGAAACCGCGACGCTGGGCTCCAG 2634
QY 653 ----- 653
Db 2635 GACCTGCTGAAGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694
QY 653 ----- 653
Db 2695 CTGTTACAGGAGACTTTGGCGGCTCGGACGCTGCTGCTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 ----- 653
Db 2755 ATTACAGACTTCGGGCTGGCTCGCTGCTGCAGATTGACGAGACAGAGTACCATGACAGAT 2814
QY 653 ----- 653
Db 2815 GGGGCAAGGTGCCATCAAGTGAATGCGCGCTGGAGTCCATTCTCCGCGCGGCTTCAAC 2874
QY 653 ----- 653
Db 2875 CACCAGATGATGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
QY 653 ----- 653
Db 2935 AAACCTTAACGATGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAGAGGGGAGCGG 2994
QY 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCACCCATTGATGTCTACATGATCATGTGTCGAATTTCTCCGCAATGGCC 3054
QY 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGTTGCTGTGTAATTTCTCCGCAATGGCC 3114
QY 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGAGCCCCAGCGCTTTGTGTATCCAGATCGAGGACTTGGCCCGCAGCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACCTTTCTACCGCTCACTGCTGGAGGACATGACATGGGGGACCTGGTGTGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3235 GAGGAGTATCTGGTACCCAGAGGGCTTCTCTGTCCAGACCTGCCCCGGGCGCTGGG 3294
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGCATGTTCCACACAGCACCGCAGCTCATCTACACAGGAGTGGCGGTGGGACCTGCACA 3354
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744

Db 3355 CTAGGGCTGGAGCCCTCTCTGAAGAGGAGGCCCCAGGTCTCTCCACTGGCACCCCTCCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGATTTGATGTGTGACTGCTGGAAATGGGGCAGCCAGAGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACATGACCCAGCCCTCTACAGGGGTACAGTGAAGGACCCCCACAGTATCCCCCTG 3534
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGCTAGTTCCTCCCTGACCTGACCTGACGCCCCCAGCTGATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCCAGATGTTGGGCCCCAGCCCTCTCGCCCCGAGAGGGCCCTCTGCTGCTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGCCTCTGGAAGGCCCAAGACTCTCTCTCCAGGGGAAGTAATGGGTC 3714
QY 845 ValLysAspValPheAlaPheGlyValAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGACGTTTTTGGCTTTTGGGGTGGCCGTGGAGAACCCCGAGTACTTGACACCCCG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGTCCCTCCAGCCCACTCTCTCTGCTTCCAGCCAGCCCTTCGACCAACCTC 3834
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACCAAGGACCCACCAAGAGGGGGGCTCCACCCAGCACCTTCAAGAGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGCGAGAGAACCCAGAGTACTGCGTCTGACAGTGCACGTGCCAGTG 3939

RESULT 6

US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-6 (1-919) x US-10-146-473-32 (1-4473)


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Qy 653 ----- 653
Db 2395 CCTGATGGGAGAAATGTGAAATTCAGTGGCCATCAAAGTGTTCAGGAAAAACACATCC 2454
Qy 653 ----- 653
Db 2455 CCCAAAGCCAAAGAAATCTTAGACGAAGCATAOGTATGGCTGTGGGTGCCCA 2514
Qy 653 ----- 653
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Db 2575 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGAAGCTTGGGCTCCGAG 2634
Qy 653 ----- 653
Db 2635 GACCTGCTGAATCGTGTATGACGATTGCCAAGGGGATGAGCTACCTGGAGATGTGCGG 2694
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Db 2695 CTCGTACACAGGACTTGGCCGCTCGGAACTGTCTGTCTGTCAGAGTCCCAACCATGTCAA 2754
Qy 653 ----- 653
Db 2755 ATTACAGACTTGGGCTGGCTCGGCTGTGGACATTTGACGAGACAGAGTACCATGCAGAT 2814
Qy 653 ----- 653
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Db 2875 CACCAGATGATGTGTGGAGTTATGCTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2934
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Qy 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCACCATGATGTCTACATGATCATGTGTCAAATGTTGGATG 3054
Qy 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCGCATGGCC 3114
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAACTGAGGACTTGGGCCCGCAGTCCCTTG 3174
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAsAla 684
Db 3175 GACAGCACCTTCTACCCCTCACTCTGAGAGACATGACATGGGGGACCTGTGTGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3235 GAGGAGTATCTGGTACCCAGAGGGCTTCTTCTGTCCAGACCTTGCCCGGGGCTGGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGCATGGTCCACACAGGCACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTGCACA 3354
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGAGGCCCTCTGAAGAGAGAGGCCCCCAAGGCTTCCATGGCACCCCTCCGAAGGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATATTTGATGTGTAACCTGGGAATGGGGGAGCCCAAGGGGCTGCANAAGC 3474
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Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGGCTAGCTTGCCTCCCTTGACCTGAGAGCCCGCCAGCTGANTATGTG 3594
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCCAGCCAGATGTTGGGCCCGCCAGCCCTTGCCTCCCGAGAGGGCCCTCTGCCTGTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGTGTGCCACTCTGGAAAGGCCCAAGACTCTCTCCCCAGGGGAAGATGGGGTC 3714
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCNAAGACGTTTTTTCCTTTTGGGGGTGCGTGGAGAACCCCGAGTACTTGACACCCAG 3774
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGTGCCTCCCTCAGCCCGCCAGCCCTCTCTCTGCTTTCAGGCCAGCTTCGACACCTC 3834
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACAGGACCCACAGCGGGGGCTCCACCAGCACCTTCAAGAGGACA 3894
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACTTGGGTCTGGACGTGCCAGTG 3939
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RESULT 7

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US-10-207-655-44
; Sequence 44: Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069, 401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44
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Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 919 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-207-655-44 (1-4473)

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Qy 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
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Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCCCAAGTGTGACCGCACAGACATGAAGCTGCGGCTCCCTTGCCTAGTCCCAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACCTGGACATGCTCCGCCACCTCTACACAGGGGCTGCCAGGTGGTGCAGGGAAACCTG 354
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Qy 61 GluLeuThrThrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACTACCTGCCCAACCAATGCCAGCCTGTCTTCTGTCAGGATATCCAGGAGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGCTACGTGCTCATGCTCACAAACAGTAGGAGGCTCCCACTGAGAGGCTGCG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTCCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCTGCTAGACAAATGGA 534
Qy 131 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCCTGTAACATACCAACCTGTCTCAGGGGCTCCCAAGGAGGCTGCGGAGCTG 594
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGGAGGGCTCTTGATCCAGCGGAACCCCG 654
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 655 CTCTGCTACAGGACACGATTTGTGGAGGACATCTTCCACAGAACCAACCCAGCTGGCT 714
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAG 774
Qy 201 GlySerArgCysTyrGlyGlnSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 775 GCTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTGTGAGGCTTGACGGCGCATGTCTGT 834
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 835 GCGGTGGCTGTGCCCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 895 GCTGCCGGCTGCAACGGGCCCAAGCACTCTGACTGCTGGCTGCCCTGCCCTTCAACCA 954
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 955 AGTGGCATCTGTGAGCTGCACTGCCCGCCAGCCTGCTCCTTACCAACAGACATTTGAG 1014
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 1015 TCCATGCCCAATCCCGAGGGCCGTATACATTCCGGCCGAGCTGTGTGACTGCTGTGCC 1074
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1075 TACAACTACCTTTCTACGAGCCTGGGATCTCGACCCCTGTCTGCCCTTGCAACCA 1134
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1135 GAGGTACAGCAGAGATGGAACACAGCGGTGTGAGAGTGACAGGCTGTGCCCGCA 1194
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1195 GTGTGCTATGGTCTGGGCATGGAGCATTTGAGAGGTGAGGGCAGTTACCACTGCCAAT 1254
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1255 ATCCAGGAGTTGCTGGCTGCAAGAGATCTTTGGGAGCCTGGCATTTCTGCCGAGAGC 1314
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
Db 1315 TTTGATGGGACCCAGCCTCCACACTGCCCTCCAGGAGGCTCCAGGAGCTCCAGTGT 1374
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
Db 1375 GAGACTCTGGAGAGATCACAGTTACTTATACATCTCAGCATGGCGGAGACGCTGCT 1434

Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1435 GACCTCAGCGCTCTTCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACAAATGCGCC 1494
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrPheLeuArgSerLeuArgGlu 460
Db 1495 TACTCGCTGACCTGCAAGGGCTGGCATCAGCTGGCTGGGCTGCGCTCACTGAGGAA 1554
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1555 CTGGGAGTGGAGTGGCTCTCATCCACCAATAACACCCACTCTGCTTCTGTCACACGGTG 1614
Qy 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1615 CCTCGGACCACTCTTTGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCCGCCA 1674
Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1675 GAGGACGAGTGTGGGGAGGGCTGGCTGCCACCACTGTGCGCCCGAGGCACTGC 1734
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1735 TGGGGTCCAGGGCCCAACCCAGTGTGCAACTGACCACTGCTTCGGGGCCAGGAGTGC 1794
Qy 541 ValGlnGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1795 GTGGAGGAATGCGGAGTACTGAGGGCTCCCGAGGAGTATGTGATGCCAGGCACTGT 1854
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1855 TTGCGCTGCCACCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGAG 1914
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1915 GCTCACCAGTGTGGCTGTGCCCACTATAAGGACCTCCCTTCTGCGTGGCCCCGTGC 1974
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1975 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAGATTTCCAGATGAGAG 2034
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 2035 GCGCATGCCAGCTTGGCCCATCAACTGCACCACTCTCTGTGTGGACCTGGATGACAAG 2094
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer- 653
Db 2095 GGCTGCCCGCGAGAGAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTGGTTGGC 2154
Qy 653 ----- 653
Db 2155 ATCTCTGCTGCTGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCGACAG 2214
Qy 653 ----- 653
Db 2215 AAGATCCGGAAGTACACAGTACGAGACTGCTGCAGGAAACGAGCTGTGTGGAGCCGCTG 2274
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Db 2455 CCCAAAGCCAAAGAAATCTTTAGAGGAAGCATACGTGATGGCTGTGGTGTGGCTCCCA 2514
Qy 653 ----- 653

Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	475	ATTGTGCGAGGCAACCAGCTCTTTGAGGACAACCTATGCCCCGTGGCGGTGTAGACAATGGA	534
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu	140
Db	535	GACCCGCTGAACAATAACACCCCTGTACAGGGGCGCTCCCCAGAGGCGCTGCGGGAGCTG	594
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	595	CAGCTTCGAGCCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGACACCCCGAG	654
Qy	161	LeuCysTyrGlnAspThrIleLeuThrPlyAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	655	CTCTGCTACCAAGGACACGATTTTGTGAAGGACATCTTCCACAAGAACCAACCACTGGCT	714
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	715	CTCACACTGATAGACACACACCGCTCTCGGGCGCTGCCACCCCGTGTCTCCGATGTGTAAAG	774
Qy	201	GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	775	GGCTCCCGCTCTCGGGGAGAGATTCTGAGGATGTTCAGAGCCTGACGGCAGCTGTCTGT	834
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	835	GCCGCTGGCTGTGCCGCTGCAAGGGGCGCACTGCCCACTGACTGCTGCCATGAGCAGTGT	894
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	895	GCTGCGCGCTGCACGGGCGCCCAAGCACTCTGACTGCCCTGGCTGCCCTTCCACTTCAACCCAC	954
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	955	AGTGGCATCTGTGAGCTGCATCTGCCAGCCCTGTGTCACTTACACACAGACAGCGTTTGAG	1014
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	1015	TCCATGCCCAATCCCGAGGGCGGTATACATTTGGCGCCAGCTGTGTGACTGTGCTGTCCC	1074
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrIleuValCysProLeuHisAsnGln	320
Db	1075	TACAACCTACCTTTCTACGGAGCTGGGATCTCTGCACCCCTGTGCTGCCCTTGCACACACAA	1134
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	1135	GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGGAAGTGCACAGAGCCCTGTGCCCGA	1194
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1195	GTGTGCTATGCTCTGGGCATGGGACACTTGCAGAGGTGAGGGGAGTTTACCAGTGCCAAAT	1254
Qy	361	IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1255	ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGAGCCTTGGGCAATTTCTGCCGAGAGC	1314
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1315	TTTGTATGGGACCCAGCCCTCCAAACACTGCCCGCTTCCAGCCAGAGAGCTCCAGAGTGT	1374
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaIleProAspSerLeuPro	420
Db	1375	CAGACTCTGGAAGAGATCACAGGTTTACCTATACATCTCAGCATGGCCGGCAGCGCTCGCT	1434
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1435	GACCTCAGCGCTCTCCAGAACCTTCGACAGTAAATCCGGGGACGAATTTCTGCACAAATGGCGCC	1494
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1495	TACTCGCTGACCTCCAAAGGCGCTGGGCATGAGCTGGCTGGGGCTGGCGCTCACTGAGGGA	1554
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480

1555	DB	CTGGGCGAGTGGACTGGCCCTCATCCACCATAACACCACCTCTGCTTGTGGACACCGGTG	1614
481	QY	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
1615	DB	CCCTGGGACCACTCTTTTCGGAAACCGCCACCAAGCTCTGCTCCACACTGCGCAACCGGCCA	1674
501	QY	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
1675	DB	GAGGACAGTGTGTGGCGAGGGCCCTGGCGCTGCGCACCGAGCTGTGGCGCCGAGGGCACTGC	1734
521	QY	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
1735	DB	TGGGGTCCAGGGCCCAACCCAGTGTGTCACTGCGAGCCAGTCTCTTGGGGCCAGGAGTGC	1794
541	QY	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
1795	DB	GTGGAGGAATGCCGAGTACTGACGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT	1854
561	QY	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
1855	DB	TTGCGGTGCCACCCCTGAGTGTGAGCCCAAGATGGCTCAGTGAACCTGTTTTGGACCGGAG	1914
581	QY	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
1915	DB	GCTGACCACTGTGTGGCCCTGTGCCCACTATAAGGACCCCTCCCTTCTGCGTGGCCCGCTGC	1974
601	QY	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620
1975	DB	CCGACGGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2034
621	QY	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
2035	DB	GGCCATGTCAGCCTTTGCCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGCAAG	2094
641	QY	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
2095	DB	GGTGTCCCGCCGAGCAGAGACGAGCCCTCTGACGTCCATCTCTCTGCGGTGGTGGTGGC	2154
653	QY	-----	653
2155	DB	ATTCTGCTGCTGTGTCTTGGGGTGGTCTTTTGGGATCTCTCATAGCGACGCGAGCAG	2214
653	QY	-----	653
2215	DB	AGATCCGGAAGTACACGATGCGGAGACTCTGTCAGGAAACGGAGCTGTGTGGAGCCGCTG	2274
653	QY	-----	653
2275	DB	ACACCTAGCGGAGCGATGCCAACGAGGGCGCAGATGCGGATCTCTGAAGAGACGGAGCTG	2334
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653	QY	-----	653
2395	DB	CCTGATGGGAGAAATGTGAATAATTCCAGTGGCCATCAAAAGTGTGTGAGGGAAACACATCC	2454
653	QY	-----	653
2455	DB	CCCAAGGCCAACAAAGAAATCTTAGACGAAGCAATACGTGATGGCTGTGTGGGCTCCCA	2514
653	QY	-----	653
2515	DB	TATGTCTCCGCTCTCTGGGCACTGCTGCTGCATCCACGGTGCAGCTGGTGCACACAGCTT	2574
653	QY	-----	653
2575	DB	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCGCGACCGCTGGGGTCCCAAG	2634
653	QY	-----	653

2635	Db	GA	CTGCTGAACTGGTGTATG	CAGATTGGCCAAAGGGGATGAGCTACCTG	GAGGATGTGGG	2694
653	Qy	----	----	----	----	653
2695	Db	CTCGTACACAGG	ACTTTGGCGCTCGGACG	TGCTGTGCTCAAGAGTCC	CAACCATGTCAA	2754
653	Qy	----	----	----	----	653
2755	Db	ATTACAGACTTCGGGCTGGCTCGGCTGTCG	CAATTGACGAGACAGAGTACC	ATGTCAGAT	2814	
653	Qy	----	----	----	----	653
2815	Db	GGGGGCAAGTGCCCATCAAGTGA	TGGCGCTGGAGTCCATTCTCCCGCGCGGTTCA	CC	2874	
653	Qy	----	----	----	----	653
2875	Db	CAC	CAGAGTGN	TGNTGGAGTTATGGTG	TGACTGTGTGGGAGCTGATCATTTTGGGCCC	2934
653	Qy	----	----	----	----	653
2935	Db	AAACCTTACGATGGGATCCAGCCCCGAGAGATCCCTG	ACTGCGAAAGGGGGAGCGG	2994		
653	Qy	----	----	----	----	653
2995	Db	CTGCCCCAGCCCCCATCTGCACCA	ATTGATGTTACATGATCATG	TGTCAAATGTTGGATG	3054	
653	Qy	----	----	----	----	653
3055	Db	ATTGACTCTG	AAATGTCGGCCAGAGATTTCGGGAGTTGGTG	TC	TGAAATTTCTCCCGCATGGCC	3114
654	Qy	----	-----	Gln	AsnGluAspLeuGlyProAlaSerProLeu	664
3115	Db	AGGACCCCCAGCGCTTTGTGGTCA	TCCAGAA	TGAGGACTTGGGCC	CAGCCAGTCCCTTG	3174
665	Qy	AspSerThrPhe	ThrArgSerLeu	LeuGluAspAspMetGlyAsp	LeuValAspAla	684
3175	Db	GACAGCACCTTCTACCGCTCACTGCTG	GAGACGATGACATGGGGGACCTG	TGTGGATGCT	3234	
685	Qy	GluGlu	TrpLeuValProGlnGlnGlyPhe	CysProAspProAlaProGlyVal	Gly	704
3235	Db	GAGAGATATCTGGTACCCAGAGGCTTCTTGT	CCAGACCTGCTCCCGGGCGCTGGG	3294		
705	Qy	GlyMetValHis	ArgHisArgSerSerThrArgSerGlyGlyGly	ValAspLeuThr	724	
3295	Db	GGCATGCTCCACACAGACCCGAGCTCATCTAC	GAGAGTGGCGGTGGGACCTGCAC	3354		
725	Qy	LeuGlyLeuGluProSerGluGluGluAlaPro	ArgSerProLeuAlaProSerGluGly	744		
3355	Db	CTAGGGCTGGAGCCCTCTGAAAGAGAGGCGCC	CCAGGCTTCCACATGGGCACCCCTCCGAAAGG	3414		
745	Qy	AlaGlySerAspValPhe	AspGlyAspLeuGlyMetGlyAla	AlaValGlyLeuGlnSer	764	
3415	Db	GCTGGCTCCGATGTATTGATGGTGACCTGG	AAATGGGGGAGCCAGAGGGGCTGC	CAAGGC	3474	
765	Qy	LeuProThrHis	AspProSerProLeuGlnArgTyrSerGlu	AspProThrValProLeu	784	
3475	Db	CTCCCCACATGACCCCGCCCTCTACAGCGGTAC	AGTGGAGACCCACAGTACCCCTG	3534		
785	Qy	ProSerGluThrAspGlyTyrValAlaProLeu	ThrCysSerProGlnProGluTyrVal	804		
3535	Db	CCCTCTGAGACTGATGGCTAGTTGTC	CCCCCTGACCTGCAGCCCCCAGCCTG	GAATATGTG	3594	
805	Qy	AsnGlnProAspValArgProGlnProProSer	ProArgGluGlyProLeuProAlaAla	824		
3595	Db	AAC	CAGCCAGATGTTGGGCCCCAGCCCCCTTCG	CCCGAGAGGGCCCTCTGCTGCTGCTGCC	3654	
825	Qy	ArgProAlaGlyAlaThrLeu	GluArgProIysThrLeuSerProGlyLys	AsnGlyVal	844	
3655	Db	CGACTGCTGCTGCATCTCTG	GAAGGCCCAAGACTCTCTCCCCAGGGAGATGG	GGCTC	3714	
845	Qy	ValLysAspValPheAlaPhe	GlyValAlaValGluAsnProGluTyrLeu	ThrProGln	864	
3715	Db	GTCA	AAAGAGGTTTGTGCTTTGGGCTTGGGGTGG	CGTGGAGAACCCGAGTACTTGGACACCC	3774	

Qy	865	GlyGlyAlaIaIaProGlnProHisProProProAlaPheSerProAlaPheAspLeu	884
Db	3775	GGAGAGCTCCCTCTAGCCCCACCTCTCTCTGCTTTCAGCCAGCTTCGACACCTC	3834
Qy	885	TyrTyrTyrAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3835	TATTACTGGAGACAGGAGCCACCAGAGCGGGGGGCTCCACCCAGACCTTCAAGGGACA	3894
Qy	905	ProThrAlaGluAsnProGluIuFyrLeuGlyLeuAspValProVal	919
Db	3895	CCTACGGCAGACAAACCCAGAGTACTCTGGGTCTGGACGTGCCAGTG	3939

RESULT 9

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US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HEREGULIN AND HER3
; FILE REFERENCE: 30448.103-US-U1
; CURRENT APPLICATION NUMBER: US/10/207.498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5

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Qy	121	AspProLeuAenAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
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Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAAGCCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	480
Qy	161	LeuCysTyrglnAspThrIleLeuTrrLysAspIlePheHisLysAsnGlnLeuAla	180
Db	481	CTCTGCTACCAGGACACAGATTTTGTGAAGGACATCTTCCACAGAACCAACCAAGCTGGCT	540
Qy	181	LeuThrIleLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTACACTGATAGACACAAACCGCTCTCGGGCTGTCCACCCCTGTGTCTCGATGTGTAG	600
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGCTCCCGCTGTGGGGAGAGATTCTAGAGATTGTTCAGAGCTTGACGGGCACGTGCTGT	660
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240
Db	661	GCCGCTGGCTGTGCCCTGTCAAGGGGCCACTGCCCCACTGACTGCTGCCATGACGAGTGT	720
Qy	241	AlaalaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GCTGCGGGCTGACAGGGGCCCAAGCACTGTGACTGCTGGCTGGCTGCCCTTCACCTTCAACCCAC	780
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTGAGCTGCATGCGCCAGCCCTGGTCACTTACAACACAGACACAGTTTGAG	840
Qy	281	SerMetProAsnProGluGlyArgTyrrPheGlyAlaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCCGAGGGCCGGTATACATTTGGGCCCAAGCTGTGTGACTGCTGCTGCC	900
Qy	301	TyrAsnThrLeuSerThrAsnValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACTACCTTTCTACGGACGTGGGATCTGTCAACCTCGTCTGCCCTCCCTGCAACACCAA	960
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	961	GAGGTGACGACGAGGATGGNACACACGGGTGTGAGAAGTGCAGCAGCCCTGTGCCCGA	1020
Qy	341	ValCysTyrglyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1021	GTGTGCTACTGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTTACCAGTGCCAAT	1080
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGGAGTTTGTCTGGCTGCGAAGAATCTTTGGGAGCCTTGGCATTTCTGCCGAGAGC	1140
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1141	TTTGATGGGGACCCAGCTCCACACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT	1200
Qy	401	GluThrLeuGluGluIleThrGlyTyrrLeuTyrrIleSerAlaTrpProAspSerLeuPro	420
Db	1201	GAGACTCTGGAAGAGATCACAGGTTACTATACATCTCAGCATGCCCGGACAGCTGCCCT	1260
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1261	GACCTCAGCGTCTTCCGAACCTCGCAAGTAAATCCGGGGAGCAATTTGCAACAATGGCGCC	1320
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1321	TACTCGCTGACCCCTGCAAGGCTGGGATATGACTTGGCTTGGGGCTGCGCTCACTGAGGGAA	1380
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
Db	1381	CTGGGCAGTGGACTGGCCCTCATCCACCAATAACCAACCCACCTCTGCTGTGTGGTGCACAGGTG	1440

Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	1441	CCCTGGGACAGAGCTCTTTTCGGAAACCCGCAACAAGCTCTGCTCCACACTGCACACCGGCCCA	1500
Qy	501	GluAspGlnCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	1501	GAGACGAGTGTGTGGCGAGGGCGCTGGCTTCACCAAGCTGTGCGCCCGAGGGGCACTGC	1560
Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1561	TGGGTTCAGGGCCCACTGAGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC	1620
Qy	541	ValGluGlnCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	1621	GTGGAGAAATGCCGAGTACTGCAGGGGCTCCCCAGGGGAGTATGTGAATGCAGGCACTGT	1680
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1681	TTGCCGTGCCACCTTGAGTGTGACGCCCAAGATGGCTCAGTGACCTGTGTTTGACCCGGAG	1740
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	600
Db	1741	GCTGACAGTGTGGCGCTGTGCCACTATAGAGACCTCCCTCTCGGTGGCCCGCTGC	1800
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	1801	CCCAGCGTGTGAAACCTGACCTCTCTACATGCCACCTCTGGAAGTTTCAGATGAGGAG	1860
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	1861	GGCGCATGCCAGCCTTGCCCATCACTGACGCCACCTCTCTGTGTGGACCTGGATGACAG	1920
Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	1921	GGCTGCCCGCCGAGCAGAGACCGACCTCTGACGTTCATCGTCTCGGTGGTGGTGGC	1980
Qy	653	-----	653
Db	1981	ATTCTGCTGGTGTGGTCTTTGGGGTGGTCTTTGGGATCCTCATAGCGACGCGCAGCAG	2040
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Db	2101	ACACTAGCGGAGCGATGCCCAACCGCGCAGATGCGGATCCTGGAAGAGACGGAGCTG	2160
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Db	2161	AGGAAGGTGAAGTGTCTGGATCTGGGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2220
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Db	2221	CCTGATGGGAGAAATGTGAATAATTCAGTGGCCATCAAAAGTGTGTGAGGGGAAACACATCC	2280
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Db	2281	CCCAAGCCAAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGTCTCCCA	2340
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Db	2461	GACCTGTGAACCTGGTGTATGCAGATTGCCAGTTGCCAAGGGGATGACCTACCTGGAGGATGTGGG	2520
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Db 2941 AGGGACCCCGCGCTTTGTGTGTCATCCAGATGAGGACTTGGSCCCAGCCAGTCCCTTG 3000
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Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACCACAGCCCGCAGCTCATCTACAGGAGTGGCGGTGGGGACCTGCACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCAGGTCTCCACTGGCACCCTCCGAAGGG 3240
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Db 3241 GCTGGCTCCGATGTTATTTGATGTGACCTGGGAATGGGGGAGCCAGCGGGCTGCCAANGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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Db 3361 CCCTCTGAGACTGATGCTACGTTGCCCTGACCTGACCTGACGCCCCAGCCCTGAATATGT 3420
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Db 3661 TATTACTGGGACCAAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGGACA 3720
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Db 3721 CCTAGCGGACGAGAACCCAGAGTACTCTGGTCTTGGACGTGCCAGTG 3765

RESULT 10
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811.123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-123-8 (1-3768)

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Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAATACCAACCCCTGTGTACAGGGGCTCCCCAGGAGGCTTGGGGAGCTG 420

QY 141 GlnLeuArgSerLeuThrGluIleLeuIysGlyValLeuIleGlnArgAsnProGln 160
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QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGACTGGCCCTCATCCACATAACACCCACCTCTGCTTGTGTGCACACGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

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QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCCCACCACTGTGTCAACTGCAGCCAGTTCTTCCGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATGCGGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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QY 601 ProSerGlyValIysProAspLeuSerTyrMetProIleTyrIysPheProAspGluGlu 620
DB 1801 CCCAGCGGTGGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCAGATGAGGAG 1860
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DB 1981 ATTCTCTGTCGTCTGTGTTGGGGTGGTCTTTTGGGATTCCTCATCAAGCGAGCGCAGAG 2040
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Db 2761 AAACCTTACGATGGATCCAGCCGGGAGATCCCTGACCTGTGGAAGGGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCAACATTCATGCTTACATGATCATGCTCAAAATGTTGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTCGGCCCAAGATTCGGGAGTTGTGTCTGAAATTCCTCCCGCATGGCC 2940
Qy 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTTGTGGTTCATCCAGATGAGGACTTGGGCCCGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGCAGATGACATGGGGGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValGly 704
Db 3061 GAGAGTATCTGGTACCCCGAGCAGGGCTTCTCTGTCCAGACCTTGGCCCGGGCGCTGG 3120
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCAATGTCACACAGCCAGCGCTCATCTACAGGAGTGGCGGTGGGACCTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCGCTCTGAAGAGGAGGCGCCCAAGGTCTCCACTGGCACCCTCCGAAAGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGATGACCTGGGAATGGGGGAGCAGAGGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCAACACATGACCCCGCCCTCTACAGGGGTACAGTGGAGNCCCAACATGCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGCTAGTGTGCCCTGACCTGACCTGACGCCCGCCAGCTGATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCAGATGTTGGCCCCCAGCCCCCTTGGCCCCGAGAGGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProGlyThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTCCACTCTGGAAGGGCCAGACTCTCTCCCGAGGAGAGATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyGlyValAlaGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAGAGCGCTTTTGGCTTTGGGGTGGCGCTGGAGAACCCCGAGTACTTGCACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCCCAGCTCTCTGCTGCTTACGCCAGCCAGCTTTCGACAACTC 3660
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCAAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAGGGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGCGCAGAGAACCCAGAGTACTTGGGTCTGGAGCTGGCCAGTG 3765

RESULT 12

US-09-984-092-3

; Sequence 3, Application US/09984092

; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P1011PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3768)
US-09-984-092-3

Alignment Scores:

Pred. No.:	0	Length:	3768
Score:	4892.00	Matches:	918
Percent Similarity:	73.15%	Conservative:	0
Best Local Similarity:	73.15%	Mismatches:	1
Query Match:	96.34%	Indels:	336
DB:	13	Gaps:	1

US-09-493-480-6 (1-919) x US-09-984-092-3 (1-3768)

Qy	1	MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla	20
Db	1	ATGAGCTGGGGCGCTTGTGCGCTGGGGCTCTCTCTCGCCCTTGTGCCCCCGAGCC	60
Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	61	GCGAGCACCCAGTGTGACCGGACACAGCATGAGCTGCGGCTCCCTGCCAGTCCCGAG	120
Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
Db	121	ACCACCTGGACATGCTCGGCACCTCTTACCAGGGCTGCCAGGTGGTGAGGAAACCTG	180
Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	181	GAACTCACTACCTGGCCGCCCAATGCCAGCGCTGCTCTTCTGCAGGATATCCAGGAGTG	240
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTACGTGCTCATGCTCACACCAAGTAGGAGGAGTCCCACTGCAGAGGCTGGCG	300
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	301	ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCCCCCTGGCGCTGTAGACAATGGA	360
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	361	GACCCGCTGAACAATATACCCCTGTCAAGGGGCGCTCCCGAGAGGCTTCGGGAGCTG	420
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAGCCCTCACAGAGATCTTGNAGAGAGGGGTCTTGATCCAGCGAGACCCCGAG	480
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGTACCAGGACACGATTTTGTGGAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
Qy	181	LeuThrIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACACCAACCGCTCTCGGGCGCTGCCACCCCTGTCTCCGATGTGAAG	600
Qy	201	GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTAGAGCTTCAGAGCTTCAGCGGCTGTCTGT	660
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240


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DB 3001 GACAGACCTTACCGCTCCTGCTGAGGAGCATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GUGUUTYRLEUVALPROGLINGLYPHEPHECYSPROASPPOALAProGLYAlaGLY 704
DB 3061 GAGGAGTATCTGTATCCCGAGGAGGGCTTCTTCTGTCAGACCTTGGCCCGGGCGCTGGG 3120
QY 705 GYMetValHisHisArgHisArgSerSerSerThrArgSerGLYGLYAspLeuThr 724
DB 3121 GGCATGGTCCACCACAGGACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTGACA 3180
QY 725 LeuGLYLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGLY 744
DB 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCATCTGCGACCTTCGAAGGG 3240
QY 745 AlaGLYSerAspValPheAspGLYAspLeuGLYMetGLYAlaAlaGLYLeuGlnSer 764
DB 3241 GCTGGCTCCGATGTATTTGATGTGACCTGGGATGGGGGAGCCAGGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
DB 3301 CTCCCCACATGACCCCGCCCTCTACAGCGGTACAGTGGAGGACCCACAGTACCCCTG 3360
QY 785 ProSerGluThrAspGLYTYRValAlaProLeuThrCysSerProGlnProGluTYRVal 804
DB 3361 CCCTCTGAGACTGATGCTACGTGCCCCCTGACCTGCGAGCCCCCAGCCCTGAATATGT 3420
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGLYProLeuProAlaAla 824
DB 3421 AACAGCCAGATGTTTGGCCCCCAGCCCCCTTGGCCCCGAGAGGGCCCTCTGCCCTGCTGCC 3480
QY 825 ArgProAlaGLYAlaThrLeuGluArgProGluPheThrLeuSerProGLYLYsAsnGLYVal 844
DB 3481 CGACCTGCTGTGCTCCTCTGGAAGGGCCCAAGACTCTCTCCCCAGGGAAGATGGGGTC 3540
QY 845 ValLYAspValPheAlaPheGLYAlaValGluAsnProGluTYRLeuThrProGln 864
DB 3541 GTCAAGACGCTTTTGTCTTGGGGGTGGCGCTGGAGAACCCCGAGTACTTGGACACCCAG 3600
QY 865 GLYGLYAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3601 GGAGGAGCTGCCCTCTAGCCCCCACCCTCTCTCTGCTTCCAGCCAGCTTCCAGACCTC 3660
QY 885 TYRTrpAspGlnAspProProGluArgGLYAlaProProSerThrPheLYsGLYThr 904
DB 3661 TATTACTGGACAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGAGCA 3720
QY 905 ProThrAlaGluAsnProGluTYRLeuGLYLeuAspValProVal 919
DB 3721 CCTACGGCAGAGAACCACAGAGTACTTGGGGTCTGGACGTGCCAGTG 3765
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RESULT 14

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US-09-877-177-11
; Sequence 11, Application US/09877177
; Publication No. US20020192652A1
; GENERAL INFORMATION:
; APPLICANT: Peter V. Danenberg et al.
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-New Gene Expression
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177-11
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Alignment Scores: 0 Length: 4530
Pred. No.: 4892.00 Matches: 918
Score:
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Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 9 Gaps: 1
US-09-493-480-6 (1-919) x US-09-877-177-11 (1-4530)
QY 1 MetGluLeuAlaAlaLeuCysArgTyrGLYLeuLeuLeuAlaLeuLeuProProGLYAla 20
DB 151 ATGAGCTGGCGGCTTGTGCGCTGGGGGCTCTCTCTCGCCCTTTGCCCGCCCGAGCC 210
QY 21 AlaSerThrGlnValCysThrGLYThrAspMetLYsLeuArgLeuProAlaSerProGlu 40
DB 211 GCAGACACCCAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTTGCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGLYCysGlnValValGlnGlnAsnLeu 60
DB 271 ACCACCTGGACATGCTCCCGCACCTCTACAGGGCTGCCAGGTGGTGAGGGAACCTG 330
QY 61 GluLeuThrTYRLeuProThrAsnAlaSerLeuSerPheLeuGlnAspPheGlnGluVal 80
DB 331 GAATCTCACCTTACCTGGCCCAATGCGAGCTGTCTCTTCTGCAAGGATATCCAGAGGTG 390
QY 81 GlnGLYTYRValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTACGTGTCTATCGCTCAACCAAGTGAAGGAGGTCCCACTGCGAGGGCTGGCG 450
QY 101 IleValArgGLYThrGlnLeuPheGluAspAsnTYRAlaLeuAlaValLeuAspAsnGLY 120
DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGACAACTATGCTCCCTGGCGGTGTAGACAATGGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGLYGLYLeuArgGluLeu 140
DB 511 GACCCGCTGAACAAATACACCCCTGTCAAGGGGCTCCCGAGAGGCTCCCGGAGGTG 570
QY 141 GlnLeuArgSerLeuThrGluLeuLYsGLYValLeuLeuGlnArgAsnProGln 160
DB 571 CAGCTTGAAGACCTTCAGAGATCTTGAAGAGGGGGTCTTGATCCAGCGGAGACCCCGAG 630
QY 161 LeuCysTYRGLNAspThrIleLeuTrpLYsAspPhePheHisLYsAsnAsnGlnLeuAla 180
DB 631 CTCTGTCTACCGAGACAGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLYs 200
DB 691 CTCACATGTATAGACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAAG 750
QY 201 GLYSerArgCysTYRGLYGLYSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GGTCTCCGCTGTGGGAGAGAGTTCAGAGATTGTTCAGAGCTTGCAGCGCTGACGGCACTGTCTGT 810
QY 221 AlaGLYGLYCysAlaArgCysLYsGLYProLeuProThrAspCysCysHisGluGlnCys 240
DB 811 GCCGTGGCTGTGCCGCTGCAAGGGGCCACTGCGCCACTGACTGCTGCTGCATGAGCAGTGT 870
QY 241 AlaAlaGLYCysThrGLYProLYsHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCGGGCTGCAGCGGCCCAAGACTCTGAGCTGCTGGCTTGGCTTCCCTTCAACCCAC 930
QY 261 SerGLYIleCysGluLeuHisCysProAlaLeuValThrTYRAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTTACACACACAGACACCGTTTGA 990
QY 281 SerMetProAsnProGluGLYArgTYRThrPheGLYAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCCAATCCGAGGGCCGATATACATTGGCGCCAGCTGTGTGACTGCTGTCTCC 1050
QY 301 TYRAsnTYRLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1051 TACAACCTACCTTTCTAGCGGACGTGGGATCTCGACCCCTCGTCTGCCCGCTGCACACCA 1110
QY 321 GluValThrAlaGluAspGLYThrGlnArgCysGluLYsCysSerLYsProCysAlaArg 340
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Db 1111 GAGGTGACAGCAGGATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCGA 1170
Qy ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db GTGTCTATGCTCTGGGCTAGGAGCACTTGGCAGAGGTGAGGCGAGTTTACAGTGCCTAAT 1230
Qy IleGlnGluPheAlaGlyCysIleValPheGlySerLeuAlaPheLeuProGluSer 380
Db ATCCAGGAGTTTGGCTGCAAGAGATCTTTGGGAGCTTGGCATTTCTGCCGAGAGC 1290
Qy PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db TTTGATGGGACCCAGACCTCCACACTGCCCGCTCCAGCCAGAGCAGCTCCAGTGT 1350
Qy GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
Db GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGTCGCGAGCAGCCTGCCT 1410
Qy AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db GACCTCAGCGTCTTCAGAACCTGCAGTAATCCGGGAGCGAATTTCTGCACATAGCGCC 1470
Qy TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
Db TACTCGCTGACCTGCAGGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGA 1530
Qy LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db CTGGCAGTGGACTGGCTCTATCACCATAACACCCACTCTGCTTCTGTGCACAGGTG 1590
Qy ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db CCCTGGGACCACTCTTCGGAAACCGCACCAAGCTCTGCTCCACACTCCCAACCGGCCA 1650
Qy GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db GAGGACAGTGTGTGGCGAGGGCTGGCTGCCACCACTGTGGCCCGAGGSCACTGC 1710
Qy TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db TGGGTCCAGGCCCCACCAGTGTGTCACTCAGCCAGTTCCTTTCGGGGCCAGGAGTGC 1770
Qy ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db GTGGAGGAATGCCAGATCTGACAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1830
Qy LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db TTGCGTGCACCTCAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG 1890
Qy AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db GCTGACCACTGTGTGGCTGTGTCCTACTAAGGACCTCTCTCTGCGTGGCCCGCTGC 1950
Qy ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db CCAGCGGTGTGAAACCTGACCTCTCTACATGCCCATCTGGAGTTTCCAGATGAGGAG 2010
Qy GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db GGCGCATGCGACCTTGGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 2070
Qy GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 553
Db GGCTGCCCCCGAGCAGAGAGCAGCCCTCTGACGTTCATTCGCTCTCTCGGTGGTGGC 2130
Qy ----- 653
Db ATTCTCTGTGTGTCTTGGGGGTGGTCTTTGGGATCTCTATCAAGCGACGGCAGCAG 2190
Qy ----- 653
Db AGATCCGGAGGTACACGATGCGGAGACTGCTGCAGGAAACGAGAGCTGTGTGGAGCCGCTG 2250

Qy 653 ----- 653
Db 2251 ACACCTAGCGGAGCGATGCCCAACAGGGCGCAGATGCGGATCTCTGAAGAGAGCGAGCTG 2310
Qy 653 ----- 653
Db 2311 AGGAAGGTGAAGTGTCTTGGATCTGGCGCTTTTGGCAGAGTCTCAAGGGCATCTGGATC 2370
Qy 653 ----- 653
Db 2371 CCTGATGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAAGTGTTCAGGGGAAACACATCC 2430
Qy 653 ----- 653
Db 2431 CCCAAGCCAAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGCTCCCCA 2490
Qy 653 ----- 653
Db 2491 TATGTCTCCGCTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGGTGTGACAGACTT 2550
Qy 653 ----- 653
Db 2551 ATGCCCTATGGTGCCTCTTAGACCATGTTCGGGAAACCCGGGACGCTGGGCTCCAG 2610
Qy 653 ----- 653
Db 2611 GACCTGTGAATGTGTGTATGCAGATTGCCAAGGGGATGAGCTACTTGGGAGGATGTGGG 2670
Qy 653 ----- 653
Db 2671 CTGTTACACAGGACTTGGCGCTGCTCGAAGCTGTGCTCAAGATGCTCCAAACCATGTCAA 2730
Qy 653 ----- 653
Db 2731 ATTACAGACTTTCGGGCTGCTCGGCTGTGGCATTTGACGACGACAGAGTACCATGAGAT 2790
Qy 653 ----- 653
Db 2791 GGGGGCAAGTGTCCCATCAGTGGATGGGCTGGAGTCCATTTCTCCGCGCGGTTCACC 2850
Qy 653 ----- 653
Db 2851 CACCAGAGTGTGTGGAGTTATGTGTGACTGTGTGGGAGCTGTATGTTGGGGCC 2910
Qy 653 ----- 653
Db 2911 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTGTGAAAGGGGAGCGG 2970
Qy 653 ----- 653
Db 2971 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATGTCAAATGTTGGATG 3030
Qy 653 ----- 653
Db 3031 ATTGACTCTGAATGTTCGGCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCAATGGCC 3090
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGAGACCCCGAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3150
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGCACTTTTACCGCTCACTGTCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3210
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3211 GAGGAGTATCTGTATCCACCCAGCAGGGCTTCTTCTGTCCAGACCTGTCCCGGGCGCTGG 3270
Qy 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3271 GGCATGGTCCACACAGGACCGCAGCTCATCTACAGGAGTGGCTGGGACCTGACA 3330

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QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3331 CTAGGGCTGAGGCTCTCTGAAGAGGAGGCCCCAGGCTCTCCACTGGCACCCTCCGAGGG 3390
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaValGlyLeuGlnSer 764
Db 3391 GCTGGCTCCCATGATATTGATGTGACCTGGGAATGGGGAGCCCAAGGGGCTGCAAGC 3450
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3451 CTCCCCACACATGACCCAGCCCTCTACAGGGGTACAGTGGAGGCCACAGTACCCTG 3510
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3511 CCCTCTGAGACTGATGCTACGTTGGCCCCCTGACCTGACGCCCCAGCCCTGAATATGTG 3570
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3571 AACGAGCAGATGTTGGCCCCAGCCCCCTTGGCCCCGAGAGGGCCCTCTGCTGTGCTGCC 3630
QY 825 ArgProAlaGlyAlaThrLeuGluArgProGlySerThrLeuSerProGlyLysAsnGlyVal 844
Db 3631 CGACTGCTGTGCCACTCTGGAAAGGGCCCCAGACTCTCTCCCCAGGGGAAGATGGGGTC 3690
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3691 GTCAAGACGCTTTTGGCTTTGGGGGTGCGGTGAGAAACCCGAGTACTTTGACACCCGAG 3750
QY 865 GlyGlyAlaAlaProGlnProHisProProProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3751 GGAGGAGCTGCCCTCAGCCCCACCCCTCTCTGCTGCTTTCAGCCGAGCCCTTCGACCACTC 3810
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3811 TATTACTGGACCAAGGACCCAGACCCAGAGCGGGGCTCCACCCAGCACCTTCAAGGGGACA 3870
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3871 CCTACGSCAGAGAACCAGAGTACTGGGTCTGGAGTGGCCAGTG 3915
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RESULT 15

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US-10-392-113-45
; Sequence 45, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
; FILE REFERENCE: 21108.000503
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45
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Alignment Scores:

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Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
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Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 13 Gaps: 1
US-09-493-480-6 (1-919) x US-10-392-113-45 (1-4530)
QY 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuAlaLeuLeuProGlyAla 20
Db 151 ATGGAGCTGGCGGCTTGTGCGGCTGGGGGCTCTCTCTGCGCCCTTTGCCCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCAGACACCCAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnLeu 60
Db 271 ACCCACTGGACATGCTCCGCCACCTCTACCAAGGGCTGCCAGGTGGTGCAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACCTACCTTACCTGCCACCAATGCCAGCTGTGCTTCTCTGCAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTGCTCATGCTCAACCAAGTGAAGGAGGTCCCACCTGCAGAGGCTGCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGTGGAGGACCCAGCTCTTTGAGGACACTATGCCCTGGCGGTGCTAGACAATGGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAATACCACTGTCTCACAGGGGCTCCCGAGGAGGCTCGGGAGCTG 570
QY 141 GluLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTGAAGGCTTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
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QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTTCCGATGTGAAG 750
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QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	QY	653	-----	653
DB	1291	TTTGATGGGACCCAGCTTCCAACTGCCCCCTCCAGCAGAGCAGCTCCAACTGTTT	1350	DB	2371	CCTGATGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAAGTGTGTGAGGAAACACATCC	2430
QY	401	GluThrLeuGluGluLeuThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420	QY	653	-----	653
DB	1351	GAGACTCTGGAAGAGATCACAGTTACTATATACATCTCAGCATGGCCGACAGCCTGCCT	1410	DB	2431	CCCAAAGCCAAACAAAGAAATCTTAGAGGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2490
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnGlyAla	440	QY	653	-----	653
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QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
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QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	QY	653	-----	653
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Qy      845   ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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GenCore version 5.1.6
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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3776	95.5	3768	2	US-08-356-786-1
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4	3776	95.5	4473	2	US-09-048-804-1
5	3776	95.5	4473	3	US-09-056-105-26
6	3776	95.5	4473	4	US-09-663-834A-3
7	3776	95.5	4530	1	US-08-229-515A-9
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9	3776	95.5	4530	4	US-09-167-322-4
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12	3776	95.5	9274	4	US-09-811-115-1

13	3632	91.9	2385	2	US-09-146-283-3	Sequence 3, Appli
14	3632	91.9	2385	3	US-08-579-823A-3	Sequence 3, Appli
15	3632	91.9	2385	3	US-09-344-195-3	Sequence 3, Appli
16	3471	87.8	1872	3	US-08-422-108-2	Sequence 2, Appli
17	3471	87.8	1872	4	US-08-432-734-2	Sequence 2, Appli
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20	1534	38.8	5532	2	US-08-475-035-3	Sequence 3, Appli
21	1534	38.8	5532	4	US-09-676-610B-17	Sequence 17, Appl
22	1451	36.7	5484	3	US-09-632-580A-3	Sequence 3, Appli
23	1451	36.7	5501	1	US-08-484-438-1	Sequence 1, Appli
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45	323.5	8.2	4989	2	US-08-666-392A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445

GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; TITLE OF INVENTION: DISIS, Mary L.

; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE

; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION

; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu

; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/625,101

; FILING DATE: 01-APR-1996

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 920010.448C7

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 1:

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RESULT 2

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; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3768
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US-08-356-786-1

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Best Local Similarity: 67.94% Mismatches: 0
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Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGGACATGCTCCGCACCTTACCGAGGCTGCCAGGTGGTGCAGGAAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAATCCTACCTACCTGCCCCACCAATGCCAGCTGTCTCTCTCTGCGAGATATCCAGGAGTG 240
Qy 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGCTACGTGTCTCATGCTCACCAACCAAGTGGAGGAGGCTCCCACTGCAGAGGCTGGGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGCAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGMAACNATACCAACCTCTGTACAGGGGCTCCCGAGAGGCTGGGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCCTCACAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTrrpLysAspIlePheHisLysAsnGlnLeuAla 180
Db 481 CTCTGCTACCAAGACACGATTTGTGAAGAGGACATCTTCCACAGAAACCAACCACTGGCT 540
Qy 181 LeuThrLeuLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGACCCCTGTCTCCGATGTGTAG 600
Qy 201 GlySerArgCysTrrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGTGGGGAGAGGTTCTGAGGATTTGTACAGGCTGACGGGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCCGGTGGCTGTGCCGCTGCAAGGGGCCCACTGCCCACTGACTGTCTGCTGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGCTGACCGGGCCCCAAGCACTCTGAGCTGCTGGCTGGCTGCCCTTCAACCTCA 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTTGGTCACTTACCAACACAGACAGCTTTGAG 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCCGAGGCGGGTATACATTCGCGGCCAGCTGTGTGACTGCTGTCCC 900
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACACTACTCTTTCTACGAGCTGGGATCTGACCTCTGCTGCCCTTGCACCAACCA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACACGACAGAGATGAAACACAGCGGTGTGAGAAGTGCAGCAAGCCTGTGCCGA 1020
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGTCTGGGCATGGAGCACTTCCGAGAGGTGAGGGCAGTTACAGTGCCTAAT 1080

Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGTGTGTGGCTGCAGAGATCTTTGGAGGCTGGCATTTCTGCGGAGAGC 1140
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGGACCCAGCTCCCACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrrpProAspSerLeuPro 420
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Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGAA 1380
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGCACTGGAGCTGGCCCTCATCCACATAACACCACTCTCTGCTTCTGCAACGGTG 1440
Qy 481 ProTrrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1441 CCTCGGACCACTCTTTTCGGAACCCGACCAAGCTCTCTCCACACTGCTCAACCCGCCA 1500
Qy 501 GluAspGluCysValGlyGluLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGTGGGCGAGGGCTGGCTGCCACCACTGTGCCGCCGAGGCACTGC 1560
Qy 521 TrrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGGTCCAGGGCCCACTCCAGTGTGTCACTGCGAGCCAGTCTCTTCCGGGCCAGGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrrpValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCGAGTACTGAGGGGGCTCCCGAGGGAGTATGTGATGATGCCAGCACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCGCTGCACCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1741 GCTGACAGTGTGTGGCTGTGCCCACTATAGGACCTCCCTCTCTGCGTGGGCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrrpLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAGGTTTCCAGATGAGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GGGCGATGCCAGCTTGGCCCATCACTGACCACTCCCTCTGTGTGGACCTGGATGACAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GGCTGCCCGCCGAGCAGAGAGCGCCCTCTGACGTCATCATCTCTGCGGTGGTGGC 1980
Qy 653 653 653 653
Db 1981 ATTCTGCTGCTGCTGCTTGGGGGTGGTCTTTGGGATCTCTCATCAAGCGACGAGCAG 2040
Qy 653 653 653 653
Db 2041 AAGATCCGAGATACAGATGCGGAGACTGCTGCAGGAAACGAGAGTGGTGGAGCCGCTG 2100
Qy 653 653 653 653
Db 2101 ACACCTAGCGGAGGATGCCCAACAGCGCAGATGCGGATCTCTGAAGAGACGAGAGCTG 2160
Qy 653 653 653 653

2161 AGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTTAAAGGGCATCTGGATC 2220
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2221 CCTGATGGGAGATGTGAAATTCAGTGGCCATCAAGTGTGAGGAAACACATCC 2280
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2281 CCCAAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGGCTCCCA 2340
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2341 TATGTCTCCCGCTTCTGGGCATCTGCCTGACATCCACGGTGACGTGGTGACACAGCTT 2400
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2401 ATGCCCTATGCTGCTCTTTAGACCATGTCGGGAAACCGGACGCTGGGCTCCAG 2460
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2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGACATTCAGACAGAGATACCATGCAGAT 2640
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2761 AAACCTTACGTTGGATCCAGCCGGGAGATCCCTGACCTGTCTGGAAGGGGGGCGG 2820
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2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGGTCAAAATGTTGGATG 2880
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2881 ATTGACTCTGAATGTGGCGCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
2941 AGGAGCCCCCAGCGCTTGTGGTCTATCCAGATGAGGACTTGGCCCCAGCCAGTCCCTTG 3000
665 AspSerThrPheTyrArgSerLeuLeuGluAspMetGlyAspLeuValAspAla 684
3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGCTGGTGTCT 3060
685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValGly 704
3061 GAGGAGTATCTGGTACCCAGCAGGGCTTCTTGTCTCAGACCCCTGCCCCCGGCGCTGGG 3120
705 GlyMetValHisArgHisArg 712
3121 GGCATGTCTCCACCAAGCAGCCCGC 3144

RESULT 3

US-09-811-115-2
: Sequence 2: Application US/09811115
: Patent No. 6632979
: GENERAL INFORMATION:
: APPLICANT: Erickson, Sharon

APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3768
TYPE: DNA
ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:

Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservatives: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

Qy 1 MetGluLeuAlaLeuCysArgTrrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCCGGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetIysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCCCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTTGGACATGCTCCGCCACTCTACACAGGGCTCCAGGTGGTGCAGGAAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GNACTCACTACCTGCCACCAATGCCAGCTGTCTCTCTGCAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATGCTCAACCAAGTGAAGGAGGCTCCCACTGCAGAGGCTGCGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCTTGGCGCTGCTAGACATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCGCTGAACAATACACCCCTGTCAAGGGGCTCTCCAGGAGGCTTGGGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuIleGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAGGCTCAGACAGATCTTGAAGAGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTrrpIysAspIlePheHisIysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACAGGACACGATTTTGTGGAGAGCATCTTCCACAGAACCAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysIys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGGCTGCCACCCCTGTCTTCCGATGTGTAG 600
Qy 201 GlySerArgCysTrrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGTCTCCGCTGCTGGGAGAGAGTTCAGAGATTTGTACAGGCTTACGCGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysIysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCCGCTGGCTGTGCCCGCTGCAGAGGGGCCACTGCGCCACTGACTGTCTGCCATGAGCAGTGT 720

Db 2881 ATTGACTCTGAATGTCGGCCCAAGATTCCGGAGTTGGTGTCTGTAATCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGACCCCCCAGCGCTTTGTGTCTCATCAGAAATGAGGACTTTGGGCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTTCTACCGCTCATCTGCTGGAGACCATGATGATGGGGGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValGly 704
Db 3061 GAGGAGTATCTGGTACCCAGAGGCTTCTTCTGTCCAGACCCCTGCCCCGGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGTTCCACACAGGCACCGC 3144

RESULT 4

US-09-048-804-1

; Sequence 1, Application US/09048804

; Patent No. 5968748

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF

; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748rls LLP

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/048,804

; FILING DATE: Herewith

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul K. Legaard

; REGISTRATION NUMBER: 38,534

; REFERENCE/DOCKET NUMBER: ISIS-2913

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4473 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Unknown

; ANTI-SENSE: No

US-09-048-804-1

Alignment Scores:

Pred. No.:

Score: 0

Length: 4473

Matches: 712

Percent Similarity: 3776.00

Best Local Similarity: 67.94%

Query Match: 95.50%

DB: 2

Gaps: 1

US-09-493-480-7 (1-712) x US-09-048-804-1 (1-4473)

Qy 1 MetGluLeuAlaAalaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20

Db 175 ATGGAGCTGGCGGCTTGTGCGCTTCTCTCGCCCTCTTGGCCCCCGAGGCC 234

Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuValArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCCCAAGTGTGCACCGGCACAGACATGAAGCTCGCGCTCCCTCCAGTCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGTGGTGCAGGAAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACCTACCTACCTGCCACCAATGCCAGCCTGTCTTCTCTGCAGGATATCCAGGAGGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTAGCTGCTCATCGCTCACCAACCAAGTGAAGGAGGTCCTCCATGTCAGAGGCTGCGG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACCACTATGCTGCTGCGCTGTAGACATGGA 534
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 535 GACCGCTGAACAATATACCACTGCTGTCAAGGGGCTCTCCAGGAGGCTGCGGAGCTG 594
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGAGGGTCTTGTATCCAGCGGAACCCCGCAG 654
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 655 CTCTGCTACAGGACCAAGATTTGTGAAGGACATCTTCCACAGAACCAACCACTGCTG 714
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGCACCCCTGTTCTCCGATGTGAAG 774
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 775 GGCCTCCGCTGCTGGGGAGAGAGTTCGTGAGGATTTGTCAAGGCTGTGACGGGCATCTGCTGT 834
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 835 GCGCGTGGCTGTGCGCGCTGCAAGGGGCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 895 GCTGCCGCTGCAAGGGGCCCCAAGCACCTCTGACTGCTGCGCTGCCCTCCACTTCAACCCAC 954
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 955 AGTGGCATCTGTGAGCTGCATGCGCCAGCCCTGGTCACTTACCAACACAGACAGCTTTGAG 1014
Qy 281 SerMetProAsnProGluGlyValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1075 TACAACTACCTTTCTAGGAGCTGGGATCTCGACCCCTGCTGCTGCCCTCCCAACCA 1134
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1135 GAGGTGCACAGCAGAGAGATGGAAACAGCGGTGTGTGAAGTGTGAGAGAGAGAGAGAGAG 1194
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Db 1195 GTGTGCTATGTGTCTGGGCATGGAGCATTGTGCGAGAGGTGAGGGCAGTTACCACTGCAAT 1254
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1255 ATCCAGGAGTTTGTGCTGGCTGCAAGAAGATCTTTGGGAGCTTGGCAATTTCTGCGCGAGAGC 1314

QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe 400
DB 1315 TTTGATGGGACCCAGCCTCCAAACATGCCCCGCTCAGCCAGAGCAGCTCCAGTGT 1374
QY 401 GluThrLeuGluGluLeuThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 1375 GAGACTCTGGGAAGAGATCACAGGTACCTATATACATCTCAGCATGGCCGAGCAGCTTGCCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACCTCAGGCTTTCAGAACCTGCAGTAATCCGGGAGAGAAATTCGCACAAATGGCGCC 1494
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DB 1495 TACTCGCTGACCCCTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisIleAsnThrHisLeuCysPheValHisThrVal 480
DB 1555 TGGGCGAGTGGACTGGCCCTCATCCACATAACACCCACCTCTGCTTGTGCACAGGTG 1614
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QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1735 TGGGTCTCAGGGGCCACCCAGTGTCAACTGAGCCAGTCTCTTCGGGGCCGAGGTGC 1794
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1855 TTGGCGTGCACCTCAGTGTGAGCCCAAGTGGCTCAGTGACCTGTTTGGACCGGAG 1914
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLeuAspProPheCysValAlaArgCys 600
DB 1915 GCTGACCAAGTGTGTGGCTGTGCCCTATAGGACCTTCCCTCTGCGTGGCCGCTGC 1974
QY 601 ProSerGlyValIleProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1975 CCCAGGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2034
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 2035 GCGCATGCGCAGCTTTGCCCATCACTGACCCACTCTGTGTGGACCTGGATGACAAAG 2094
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer- 653
DB 2095 GGCTGCCCCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCATCTCTCGGTGGTGGC 2154
QY 653 ----- 653
DB 2155 ATTCTGCTGTCGTCTTGGGGTGGTCTTTGGGATCTCTCATCAAGCGCGGAGCAG 2214
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DB 2215 AAGATCCGGAAGTACACGATCGGAGACTGCTGCAGGAACCGAGCTGTGGAGCGCGCTG 2274
QY 653 ----- 653
DB 2275 ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGGGATCTCTGAAGAGCGGAGCTG 2334
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DB 2395 CCTGATGGGAGAAATGTGAAAAATTCAGTGGCCATCAAAAGTGTGTGGGGAACACATCC 2454
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DB 2455 CCCAAAGCCNACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCA 2514
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DB 2755 ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGACAGACAGTACCATGCAGAT 2814
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DB 2875 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2934
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DB 2935 AAACCTTACGATGGGATCCAGCCCGGGAGATCCCTGACCTGTGTGGAAGGGGAGCGG 2994
QY 653 ----- 653
DB 2995 CTGCCCCAGCCCCCATCTGCACCATGTGATGTCTACATGATCATGTGTCAAATGTGGATG 3054
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QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 3115 AGGGACCCCGCGCTTTGTGGTCAATCCAGATGAGGACTTGGGCCCGAGCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
DB 3175 GACAGCACCTTCTACCGCTCACTGTCTGGAGGACGATGACATGGGGACCTGGGTGGATGCT 3234
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DB 3235 GAGGAGTATCTGTGATCCCGACGAGGCTTCTTCTGTCCAGACCTGTCGCCCGGGGCTGG 3294
QY 705 GlyMetValHisArgHisArg 712
DB 3295 GGCATGGTCCACCAAGGACCGC 3318

RESULT 5

US-09-056-105-26
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221

QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 2035 GCGCATGCCAGCTTGGCCCATCAACTGACCCCACTCTCTGTGGACCTGGATGACAAG 2094
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
DB 2095 GGTGCCCCCGCGAG 2154
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DB 2155 ATTCTGT 2214
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DB 2215 AAGATCCGGAGTACACGATGGGAGACTGCTGCAGGAAACGGAGCTGTGTGGAGCGCTG 2274
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DB 2275 ACACCTAGCGGAGGATGCCCAACACGAGCGCAGATGCGGATCTGTAAAGAGAGAGCTG 2334
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DB 2335 AGGAAGTGAAGTGTCTGTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2394
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DB 2395 CCTGATGGGAGATGTGAATTCAGTGGCCATCAAGTGTGTGAGGAAACACATCC 2454
QY 653 ----- 653
DB 2455 CCCAAGCCAAAGAAATCTTAGCAAGCATACGTGATGGTGTGTGGCTTCCCA 2514
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DB 2515 TATGTCTCCCGCTTCTGTGGGCATCTGCTGATCCAGTGCAGTGTGTGACAGCTGTGTG 2574
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DB 2575 ATGCCCTATGGTGTCTTAGACCATGTCCGGGAAACCGGGAGCGCTGGGCTCCAG 2634
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QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664

DB 3115 AGGACCCCCAGCGCTTTGTGTGTATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
DB 3175 GACAGACCTTCTACCGCTCACTGCTGGAGGAGATGACATGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3235 GAGGAGTATCTGTACCCAGCAGGGCTTCTTCTGTCTCCAGACCTTGCCTCCGCGCTGG 3294
QY 705 GlyMetValHisAspGHisArg 712
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RESULT 6
US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; NUMBER OF SEQ ID NOS: 2000-09-15
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)....(3942)
US-09-663-834A-3
Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
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QY 1 MetGluLeuAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTCGGCTCTCCAGTCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 295 ACCCACTTGAATGCTCGCCACCTCTACCAAGGCTGCGAGTGTGTCAGGAGAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspLleGlnGluVal 80
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DB 475 ATTGTGGAGGAGCCAGCTCTTTGAGGACAACTATGCTCTGGCCCTGTGTAGCAATGGA 534
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 535 GACCCGCTGACACATACACACCTCTGTACAGGGGCTCTCCCGAGGAGGCTGCGGAGCTG 594

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1231 ATCCAGAGTTTGTGTGCTGCAGAGATCTTTGGAGCTTGGCATTTCTGCCGGAGAGC 1290
381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
1291 TTTGATGGGACCCAGCCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCAAAGTGT 1350
401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
1351 GAGACTCTGGAAGAGATCACAGGTGTACCTATATACATCTCAGCATGGCCGAGCAGCTGCCT 1410
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1471 TACTCGCTGACCTTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTCAGGGAA 1530
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1651 GAGCAGGAGTGTGGGCGAGGGCTGGCCCTGCCACAGCTGTGCCCGCGAGGCGACTGC 1710
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1831 TTGCGGTGCCACCTGAGTGTGAGCCCGCAGAAATGGCTCAGTGACCTGTGTTGGACCGGAG 1890
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601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
1951 CCCAGCGGTGTGAACCTGACCTCTCTACATGTCCTCATCTGGAAGTTCGATGAGGAG 2010
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641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653

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654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
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Db 1411 |||||GACCTCAGCGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCGAAATCTTGCAATGGCGCC 1470
Qy 441 |||||TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 |||||TACTCGCTGACCTCTGCGAGGGCTGGGATCAGCTGGCTGGGCTGCCCTCACTGAGGAAA 1530
Qy 461 |||||LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1531 |||||CTGGCAGTGAAGCTGGCGCTCATCCACATAACACCCACCTCTGCTTGGTGACACCGTG 1590
Qy 481 |||||ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1591 |||||CCCTGGAGACAGCTCTTTCGAAACCCCGCACCAAGCTCTGTCTCCACACTGCGCAACCGGCCA 1650
Qy 501 |||||GluAspGlnCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1651 |||||GAGCAGAGTGTGTGGCGAGGGCTGGCTGCGCAGCTGTGGCTGGCGCGGCGCACTGC 1710
Qy 521 |||||TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1711 |||||TGGGGTCCAGGGCCCCACCTGAGTGTCACTGCGAGCCAGTTCTTTCGGGCGCAGGAGTGC 1770
Qy 541 |||||ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAlaAlaArgHisCys 560
Db 1771 |||||GTGGAGGAATGCGCAGTACTGCGAGGGCTCCCGCAGGAGTATGTGAATGCCAGGCACTGT 1830
Qy 561 |||||LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1831 |||||TTCCCGTGCACCCCTGAGTGTGCGCAGCCAGAAATGGCTCAGTGACCTCTCTTCTGGGCGCGCTGC 1890
Qy 581 |||||AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1891 |||||GCTGACCAAGTGTGTGGCTGTGCCACTATAGGACCTCTCCCTTCTGGGTGGCGCGCTGC 1950
Qy 601 |||||ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1951 |||||CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCCATCTGGAAGTTTCCAGATGAGGAG 2010
Qy 621 |||||GlyValCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 2011 |||||GGCGCAGCCAGCCTTGCCCCATCACTGACCCACCTCTCTGTGTGGACCTGGATGACAG 2070
Qy 641 |||||GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 2071 |||||GGCTGCCCGCCGAGCAGAGCCAGCCCTCTGAGCTCCATCGTCTCTGCGGTGGTTGGC 2130
Qy 653 ----- 653
Db 2131 |||||ATTCTGCTGCTGTGTGGGGTGGTCTTTGGGATCTCATCAGCGACGCGCAGCAG 2190
Qy 653 ----- 653
Db 2191 |||||AAGATCGGAAGTACACAGATGCGGAGACTGTCTGAGGAAACCGGAGCTGTGGAGCCGCTG 2250
Qy 653 ----- 653
Db 2251 |||||ACACTAGCGGAGGATGCCAACCGAGCGCAGATGCGGATCTGGAAGAGAGCGGAGCTG 2310
Qy 653 ----- 653
Db 2311 |||||AGGAAGTGAAGTGTGTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2370
Qy 653 ----- 653
Db 2371 |||||CTGTATGGGAGAAATGTGAATAATTCAGTGGCCATCAAGTGTGAGGGAACACATCC 2430
Qy 653 ----- 653
Db 2431 |||||CCCAAGCCAAACAGAAATCTTAGCAGCAACATACGTGATGGTGTGTGGGTCCCCA 2490
Qy 653 ----- 653

Db 2491 |||||TATGTCTCCCGCCTTCTGGGGAATCTGCTGACATCCACGGTGCAGCTGTGTGACACAGCTT 2550
Qy 653 ----- 653
Db 2551 |||||ATGCCCTATGGCTGCCTCTTAGACCAATGTCCGGGAAACCGCGGACGCTTGGGCTCCAG 2610
Qy 653 ----- 653
Db 2611 |||||GACCTGCTGAATGGTGTATGATGAGATTGCCAAGGGGATGAGCTACCTGAGAGATGTGGG 2670
Qy 653 ----- 653
Db 2671 |||||CTCGTACACAGGAGACTTGGCGGCTCGGAACTGTGCTGTGCTCAAGAGTCCCAACCATGTCAA 2730
Qy 653 ----- 653
Db 2731 |||||ATTACAGACTTGGGGCTGGCTCGGCTGTGACATTGACGAGACAGAGTACCATGCAGAT 2790
Qy 653 ----- 653
Db 2791 |||||GGGGGCAAGGTGGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTTACC 2850
Qy 653 ----- 653
Db 2851 |||||CACAGAGTGAATGTGTGGAGTTATGTGTGAGTGAATGTGTGGGAGCTGATGACTTTTGGGGCC 2910
Qy 653 ----- 653
Db 2911 |||||AAACCTTACGATGGATCCCGAGCCCGGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG 2970
Qy 653 ----- 653
Db 2971 |||||CTGCCCCAGCCCCCATCTGCAACCATGATGTCTACATGATCATGTGTCAAATGTTGGATG 3030
Qy 653 ----- 653
Db 3031 |||||ATTGACTCTGAATGTGGCCCAAGATTCGGGAGTGTGTCTGTAATTTCTCCGCAATGGCC 3090
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 |||||AGGGACCCCGCAGCGCTTTGTGGTCAATCCAGATGAGGACTTGGGCGCCAGCTCCCTTG 3150
Qy 665 |||||AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 |||||GACAGCACTTCTACCGCTCACTGCTGGAGACCATGACATGGGGGACCTGTGTGATGCT 3210
Qy 685 |||||GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3211 |||||GAGAGTATCTGGTACCCCGAGGAGGCTTCTTCTGTCCAGACCTTGGCCCCGGGCTGGG 3270
Qy 705 |||||GlyMetValHisArgHisArg 712
Db 3271 |||||GGCATGTCCACACAGCGACCGC 3294

RESULT 9

US-09-167-322-4

; Sequence 4, Application US/09167322

; Patent No. 6365151

; GENERAL INFORMATION:

; APPLICANT: Allegheny University of the Health

; Sciences, Halpern, Michael S.

; England, James M.

; TITLE OF INVENTION: CANCER VACCINE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

; STREET: Suite 1800, Two Penn Center Plaza

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/167,322
 FILING DATE: 07-Oct-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/00582
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 REGISTRATION NUMBER: 30,480
 REFERENCE/DOCKET NUMBER: 7933-33 PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4530 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-167-322-4
 Alignment Scores:
 Pred. No.: 0 Length: 4530
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-167-322-4 (1-4530)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla 20
 DB 151 ATGGAGCTGGCGGCTTGGCGGCTGGCGGCTCTCTCGCCCTCTTGGCCCCCGAGGC 210
 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 211 GCGAGACCCAGTGTGACCCGGCACAGCATGTAAGCTCGGCTCCCTGCCAGTCCCGAG 270
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 271 ACCCACTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGAAACCTG 330
 QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 DB 331 GAACTCACCTTACCTGCCACCAATGCGAGCTGTCTCTCGAGGATATCCAGGAGGTG 390
 QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 391 CAGGGCTAGTGTCTATCCTCACACCAAGTGGAGGAGTCCCACTGCAGAGGCTGCGG 450
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 DB 451 ATTGTGGAGGACCCAGCTCTTTGAGGACCACTATGCTCCCTGGCCGTGTAGACAATGGA 510
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 511 GACCGCTGAACAATACCAACCCCTGTGCAGAGGGGCTTCCAGGAGGCTTGGGGAGCTG 570
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 571 CAGCTTCGAAGCTCTCAAGATCTTGAAGGAGGGGGTCTTGTATCCAGCGGAACCCCGAG 630
 QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
 DB 631 CTCTGTACAGGACACGATTTGTGAAGGACATCTTCCACAAAGAAACCAACAGCTGGCT 690
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200

DB 691 CTCACATGATAGACACCAACCGCTCTCGGGCTGCGCCCTGTTCTCGATGTGTAG 750
 QY 201 GlySerArgCysTrpGlyLeuSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 751 GCGTCCCGCTGCTGGGGAGAGAGTCTCAGAGATTGTACAGAGCTGACGGCGCATGTCTGT 810
 QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
 DB 811 GCGGCTGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 870
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 871 GCTGCGGCTGACAGGGCCCCAAGCACTCTGACTGCTGGCTGCTCCCTTCAACCCAC 930
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 DB 931 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCCACTACACACACAGACAGTTGAG 990
 QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
 DB 991 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTGCC 1050
 QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 DB 1051 TACAACCTACTTCTACGGAGCTGGGATCTCGACCTCTGTGCCCCCTGTCACACCA 1110
 QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 DB 1111 GAGGTGACACGACGAGGATGGACACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCGA 1170
 QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 DB 1171 GTGTGCTATGTGCTGGGCAATGAGCACTTGCAGAGGTGAGGGCAGTTACCATGTGCCAAT 1230
 QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 DB 1231 ATCCAGAGTTTGTGCTGGCTGCAGAGAGATCTTTGGGAGCTTGGCATTTCTGCCGAGAGC 1290
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1291 TTTGATGGGACCCAGCTCCAACTGCCCCGCTCCAGCGAGCAGCAGCTCCAAAGTGT 1350
 QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaThrProAspSerLeuPro 420
 DB 1351 GAGACTCTGCAAGAGATCACTGCTTACCTATACATCTACAGCATGGCCGAGCAGCTGCT 1410
 QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala 440
 DB 1411 GACCTCAGGCTCTTCCAGAACCTGCAGATATCCGGGGAGCAATTTCTGCACATGGCGCC 1470
 QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
 DB 1471 TACTGCTGACCTGTCNAGGGCTGGGCATCAGCTGGCTGGGCTGGGCTCACTGAGGGAA 1530
 QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
 DB 1531 CTGGGAGTGGAGTGGCCCTCATCCACCATTAACCCACCTCTGCTGTGTCGACACCGGTG 1590
 QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 DB 1591 CCTGGGACACAGCTCTTTCGGAAACCCGACCAAGCTCTGCTCCACACTGCGCAACCGGCCA 1650
 QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 DB 1651 GAGGACAGTGTGTGGCGAGGGCTGGCTGCTGCACAGCTGTGCGCCCGAGGGCACTGC 1710
 QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGlnCys 540
 DB 1711 TGGGGTCCAGGGGCCCAACCCAGTGTGTCAACTGCGAGCAGTCTCTTCCGGGGCCAGGAGTGC 1770
 QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560

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Db 1771 GTGAGGAATGCCAGTACTGCAGGGGCTCCCGAGGAGTATGTGATGCCAGCACTGT 1830
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1831 TTGCGGTGCCACCTGAGTGTGCAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG 1890
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProPheCysValAlaArgCys 600
Db 1891 GCTGACCAAGTGTGGGCTGTGGCCCTATTAAGACCCCTCCCTTCTGGGTGGCCCGCTGC 1950
Qy 601 ProSerGlyValIysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1951 CCACGGGTGTAAACCTGACCTCTCTACATGCCATCTGGAAGTTTCCAGATGAGGAG 2010
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 2011 GGCGCATGCCAGCCTTGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 2070
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 2071 GGCTGCCCGCCGAGCAGAGCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC 2130
Qy 653 ----- 653
Db 2131 ATTCTGCTGTGTGTCTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGAG 2190
Qy 653 ----- 653
Db 2191 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAGCGAGCTGGTGGACCGCTG 2250
Qy 653 ----- 653
Db 2251 ACACCTAGCGGAGGATGCCCAACAGCGCGAGATGCGATCCTGAAAGAGACGGAGCTG 2310
Qy 653 ----- 653
Db 2311 AGNAGTGAAGTGTCTTGATCTGTGGCGCTTTTGGCACAGTCTCAAGGGGATCTGGATC 2370
Qy 653 ----- 653
Db 2371 CCTGATGGGAGAATGTGAAATTTCCAGTGGCCATCAAGTGTGGAGGAACACATCC 2430
Qy 653 ----- 653
Db 2431 CCNAAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGCTGTGGTGGCTCCCCA 2490
Qy 653 ----- 653
Db 2491 TATGTCTCCCGCTTCTGGGCGATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2550
Qy 653 ----- 653
Db 2551 ATGCCCTATGCTGCTCTTAGACCATGTCCGGGAAACCGCGAGCCCTGGGCTCCAG 2610
Qy 653 ----- 653
Db 2611 GACCTGTGAACCTGTATGCAGATTCGCAAGGGGATGAGTACCTGGAGGATGTGCGG 2670
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Db 2671 CTGTAACAGGACTTTGGCGCTTCGGAGCGTGTGCTGAGAGTCCCAACCATGTCAAA 2730
Qy 653 ----- 653
Db 2731 ATTACAGACTTGGGCTGGCTCGCTGCTGTCATTCAGCAGACAGAGTACCATGCAGAT 2790
Qy 653 ----- 653
Db 2791 GGGGGCAAGGTGCCATCAAGTGTGATGGCGTGGAGTCCATTTCTCCGCGCGGTTTCAAC 2850
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Db 2851 CACAGAGTGAATGTGGAGTTATGTGTGCTGCTGTGGGAGCTGATGATCTTTTGGGGCC 2910
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Qy 653 ----- 653
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Qy 653 ----- 653
Db 3031 ATTGACTCTGAATCTCGSCCAAGATTCCGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3090
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGACACCCCGAGCGCTTTGTGTCATCCAGAATGAGGACTTTGGGCCCGACGCTCCCTTG 3150
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGCACCTTCTACCCGCTCACTGCTGGAGACGATGATGATGGGGACCTGTTGGATGCT 3210
Qy 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
Db 3211 GAGGATATCTGTATCCCGACGAGCGGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGG 3270
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RESULT 10

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US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527.487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1
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Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-527-487-1 (1-4530)

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Qy 1 MetGluLeuAlaLeuLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 151 ATGAGGTGGCGGCTTTGTGCGGCTGGGGGTCTCTCTCGCCCTCTTCCCGCCCGAGCC 210
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetIysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCAAGTGTGACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 270
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCCACCTGGACATGCTCCGCCACTCTACCGAGGCTGCCAGGTGTGCAGGGAACCTG 330
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
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QY 653 ----- 653
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QY 653 ----- 653
Db 2671 CTGCTACACAGGACTTGGCGCTCGGAACGTGCTGCTCAAGAGTCCCAACCATGTCAA 2730
QY 653 ----- 653
Db 2731 ATTACAGACTTGGGGCTGGCTCGGCTGCTGACATTCACGAGACAGATGACATGACAGAT 2790
QY 653 ----- 653
Db 2791 GGGGGCAAGGTGCCCATCAAGTGTGATCGGCTGGAGTCCATTCTCCCGCGCGGTTTCA 2850
QY 653 ----- 653
Db 2851 CACCAGAGTGTATGTCGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGCGC 2910
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Db 2911 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAAGGGGAGCGG 2970
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QY 653 ----- 653
Db 3031 ATTGACTCTGAATGTCGGCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCGATGCC 3090
QY 654 ----- GluAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGAGCCCCAGCGCTTTGTGTCTATCCAGAAATGAGGACTTGGGCCCCAGCGCTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGCACCTCTTACCCCTACTCTGAGAGCAGTACATGAGGGGACCTGGTGGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3211 GAGGAGTATCTGTTACCCAGCAGCGCTTCTTCTGTCCAGACCTTGCCCCGGGCGCTGG 3270
QY 705 GlyMetValHisHisArgHisArg 712
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RESULT 11

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US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11
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Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
Db: 4 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-877-177A-11 (1-4530)

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QY 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
Db 151 ATGAGAGTGGCGGCTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGCCCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCCCAAGTGTGCACCGGCACACATGAAGCTGGCGCTCCCTGCGAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValLeu 60
Db 271 ACCCAGCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACCTCACCTACCTGCCCAATGCCAGCTGTCTCTCTGCGAGATATCCAGGAGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTGCTCATCGCTCACCAAGTAGGAGGAGTCCCACTGCAGAGGCTGCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValIleAspAsnGly 120
Db 451 ATTGTGGAGGACACCCAGCTCTTTGAGGACAACTATGCCCCCTGGCCGTGTAGCAATGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACATACCAACCCCTGTACAGGGGCTCCCAAGGAGGCTGCGGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAGACCCCAAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACCAAGGACACGATTTTGTGAAGAGACATCTTCCACAGAAACAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAG 750
QY 201 GlySerArgCysThrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GCGTCCGCTGCTGGGAGAGAGATTCTGAGGATTTGTACAGAGCTGACGCGCACTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 811 GCGGCTGCTGTGCCGCTGCAAGGGCCACTGCCCACTGTCTGCTCCATGACAGAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTGCGGCTGACCGGGCCCCAAGCACTCTGACTGCCCTGGCTGCTCCACTTCAACCAAC 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrThrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTTACCAACACAGACACGTTGAG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCGGTATACATTTGGCGCGCAGCTGTGTGACTGCTGTCTCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1051 TACAACTACCTTTCTACGAGAGTGGATCTTGCACCTCTGCTGCTGCCCTGCAACACCAA 1110
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QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerIysProCysAlaArg 340
Db 1111 GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCGA 1170
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Db 1171 GTGTCTATGTGCTGGCGATGAGACATTTGCGAGAGGTGAGGCGAGTTACCAAGTGCCAT 1230
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGGAGCTTGCCATTTCTGCGGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
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QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
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Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys	640
Db	3591	GGCGCATGCCAGCCTTCCCCCATCACTGCACCACTCTGTGTGAACCTGTGATGACAG	3650
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Db	4371	GGGGCAAGGTGCCCATCAAGTGAATGGCGCTGGAGTCCATTCTTCGCCGCGGTTCA	4430
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Db	4551	CT	GGCCAG	CCCCC	CCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGGATG	4610
Qy	653	----	----	----	653	
Db	4611	ATT	GACTCT	GAATGTGG	CCACAATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	4670
Qy	654	----	----	-----	-----	654
Db	4671	AG	GAACCC	CCCCC	CGCTTTTGTGTCATCCAGATGAGGACITTTGGCCCCAGCCAGTCCCCTTG	4730
Qy	665	App	SerThr	PheTyr	ArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	4731	GAC	AGCAC	CTTCTAC	CGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT	4790
Qy	685	Glu	CluTyr	TrpLeuValPro	GlnGlnGlyPhePheCysProAspProAlaProGlyValaGly	704
Db	4791	GAG	GAGAT	ATCTGGT	TACCCAGCAGCGGTCTTCTGTCTCAGACCTGCCCCCGGGCCTGGG	4850
Qy	705	Gly	MetVal	HisHisArgHisArg	712	
Db	4851	GGC	ATG	TGTCAC	CACAGGACCGC	4874
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US-09-146-283-3						
; Sequence 3, Application US/09146283						
; Patent No. 5976546						
; GENERAL INFORMATION:						
; APPLICANT: Laus, Reiner						
; APPLICANT: Ruegg, Curtis L.						
; APPLICANT: Wu, Hongyu						
; TITLE OF INVENTION: Immunostimulatory Compositions						
; NUMBER OF SEQUENCES: 10						
; CORRESPONDENCE ADDRESS:						
; ADDRESSEE: Dehlinger & Associates						
; STREET: 350 Cambridge Ave. Suite 250						
; CITY: Palo Alto						
; STATE: CA						
; COUNTRY: USA						
; ZIP: 94306						
; COMPUTER READABLE FORM:						
; MEDIUM TYPE: Floppy disk						
; COMPUTER: IBM PC compatible						
; OPERATING SYSTEM: PC-DOS/MS-DOS						
; SOFTWARE: PatentIn Release #1.0, Version #1.25						
; CURRENT APPLICATION DATA: US/09/146,283						
; FILING DATE: 03-SEPT-1998						
; CLASSIFICATION: 536						
; ATTORNEY/AGENT INFORMATION:						
; NAME: Judge, Linda R.						
; REGISTRATION NUMBER: 42,702						
; REFERENCE/DOCKET NUMBER: 7636-0010.21						
; TELECOMMUNICATION INFORMATION:						
; TELEPHONE: 650-324-0880						
; TELEFAX: 650-324-0960						
; INFORMATION FOR SEQ ID NO: 3:						
; SEQUENCE CHARACTERISTICS:						
; LENGTH: 2385 base pairs						
; TYPE: nucleic acid						
; STRANDEDNESS: double						
; TOPOLOGY: linear						
; MOLECULE TYPE: DNA (genomic)						
; HYPOTHETICAL: NO						
; ANTI-SENSE: NO						
; ORIGINAL SOURCE:						

ORGANISM: homo sapiens
 INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
 US-09-146-283-3

Alignment Scores:

Pred. No.: 0 Length: 2385
 Score: 3632.00 Matches: 659
 Percent Similarity: 98.65% Conservative: 0
 Best Local Similarity: 98.65% Mismatches: 5
 Query Match: 91.86% Indels: 4
 DB: 2 Gaps: 2

US-09-493-480-7 (1-712) x US-09-146-283-3 (1-2385)

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 Db 191 GNACTCACTACCTGCCCAATGCCAGCTGTCTCTCTGCAAGGATATCCAGAGGTG 250
 Qy 81 GlnGlyTrpValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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Qy 301 TyrAsnTrpLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisGln 320
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RESULT 15

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US-09-344-195-3
; Sequence 3, Application US/09344195
; Patent No. 6210662
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
;             Ruegg, Curtis L.
;             Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSP-HER-2 fusion gene; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-344-195-3
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Alignment Scores:
Pred. No.: 0 Length: 2385
Score: 3632.00 Matches: 659
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 5
Query Match: 91.86% Indels: 4
DB: 3 Gaps: 2
US-09-493-480-7 (1-712) x US-09-344-195-3 (1-2385)
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Qy 1 MetGluLeuAlaLeuCysArgGlyTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
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Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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Search completed: June 7, 2004, 15:45:45
Job time : 251.414 sec

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 7, 2004, 13:54:19 ; Search time 643.463 Seconds
(without alignments)
5047.907 Million cell updates/sec

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Perfect score: 3954
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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RESULT 1
US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; FILE REFERENCE: 30448.103-US-UI
; CURRENT APPLICATION NUMBER: US/10/207,498
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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3	3776	95.5	3768	9	US-09-811-115-2	Sequence 2, Appli
4	3776	95.5	3768	9	US-09-854-356-9	Sequence 9, Appli
5	3776	95.5	3768	9	US-09-930-125-1	Sequence 1, Appli
6	3776	95.5	3768	13	US-09-984-092-3	Sequence 3, Appli
7	3776	95.5	3768	13	US-10-280-576-3	Sequence 3, Appli
8	3776	95.5	3768	13	US-09-765-973-1	Sequence 1, Appli
9	3776	95.5	3768	15	US-10-313-644-1	Sequence 1, Appli
10	3776	95.5	4473	10	US-09-441-411-5	Sequence 5, Appli
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33	3521	89.0	2132	16	US-10-412-804A-3	Sequence 3, Appli
34	3205	81.1	3955	9	US-09-870-759-117	Sequence 117, App
35	3205	81.1	3955	9	US-09-854-356-10	Sequence 10, Appli
36	3205	81.1	3955	10	US-09-751-708A-117	Sequence 117, App
37	3189.5	80.7	3771	9	US-09-854-356-11	Sequence 11, Appli
38	2497.5	63.2	1479	16	US-10-412-804A-1	Sequence 1, Appli
39	1650	41.7	2091	9	US-09-821-883-9	Sequence 9, Appli
40	1630.5	41.2	2070	9	US-09-821-883-7	Sequence 7, Appli
41	1614.5	40.8	1692	9	US-09-821-883-8	Sequence 8, Appli
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ALIGNMENTS

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; NAME/KEY: CDS
; LOCATION: (1)... (3765)
US-10-207-498-5

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Alignment Scores:

Alignment Scores:			
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Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	15	Gaps:	1

US-09-493-480-7 (1-712) X US-10-207-498-5 (1-3765)

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Db	181	GAACTCACCTACCTGCCACCAATGCCAGCTGTCTCTCTCGAGATATCCAGGAGTG	240	
Qy	81	GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg	100	
Db	241	CAGGGCTACGTGCTCATCGCTCACACCAAGTGAAGCAGTCCCACTGCAGAGGCTCGCG	300	
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Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140	
Db	361	GACCGCTGAACATACACACCCCTGTCTCAGGGGCTGCCAGGAGGCTCGCGGAGCTG	420	
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160	
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Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200	
Db	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAG	600	
Qy	201	GlySerArgCysTrpGlyGlnSerSerGluAspCysGlnSerLeuThrArgThrValCys	220	
Db	601	GGCTCCCGCTGCTGGGAGAGATTTCTGAGGATGTCTCAGAGCTCAGCGGCATCTGTCTGT	660	
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240	
Db	661	GCCGCTGGCTGTGCCCGCTGCAAGGGGCCATGTGCCCACTGACTGCTGCATGAGCAGTGT	720	
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	
Db	721	GCTGCGGGCTGACGGGCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCAACCCAC	780	
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	
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Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
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Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
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Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
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Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1261	GACCTCAGCGCTTCTCCAGAACCTCCAGATTAATCCGGGACGATCTTCGACCATGGCGCC	1320
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1321	TACTCGCTGACCTTCGAAGGCTGGGCATCAGCTGGCTGGCGCTGCGCTCACTGAGGGAA	1380
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
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Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
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Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
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Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	1621	GTGGAGGAATGCCGAGTACTTGCAGGGCTCCCGCAGGAGGATATGTGAATGCCAGGACATGT	1680
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
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Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrIleYsAspProPheCysValAlaArgCys	600
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Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluclu	620
Db	1801	CCCAGCGGTGTGAACCTGCACCTCTCTCTACATGCGCCATCTGGAGATTTCCAGATGAGGAG	1860
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
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Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer-----	653
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Db 2281 CCGAAGCCAAAGAAATCTTAGACGAGCATACGTGATGCTGGTGTGGGCTCCCA 2340
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Db 2341 TATGCTCCCGCTTCTGGGCATCTGCTGACATCCAGGTGCAGCTGGTGACACAGCTT 2400
QY 653 ----- 653
Db 2401 ATGCCCTATGGCTGCTCTTAGACATGTCGCGAAGAACCGCGAGCGCTGGGCTCCAG 2460
QY 653 ----- 653
Db 2461 GACCTGTGAAGTGTGTATGCAGATTCCAAAGGGATGAGCTACCTGGAGGATGTGGG 2520
QY 653 ----- 653
Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGCTGCTCAAGAGTCCCAACCATGTCAA 2580
QY 653 ----- 653
Db 2581 ATTACAGACTTGGGCTGGCTGGCTGTGACATTGACGAGACAGAGTACCATGCAGAT 2640
QY 653 ----- 653
Db 2641 GGGGGCAAGTGCCCATCAAGTGGATGCGGCTGGATGCTTCTCCGCGCGGCTTCAAC 2700
QY 653 ----- 653
Db 2701 CACCAGAGTGATGTGTGAGTATATGTTGATGCTGTGTGGAGCTGATGACTTTTGGG 2760
QY 653 ----- 653
Db 2761 AACCTTACGATGGATGCCAGCCCGGAGATCCCTGACCTGTGGAAAGGGGAGCGG 2820
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Db 2821 CTGCCCCGCCCCCATCTGCACCATTTGATGCTTACATGATCATGCTCAATATGTTGATG 2880
QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGCAAGATTCGGGAGTGTGTCTGAATTTCTCCCGCATGCGC 2940
QY 654 ----- 664
Db 2941 AGGACCCCCAGCGCTTGTGGTCAATCCAGAAATGAGGACTTGGGCCCCAGCGATCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
3001 GACAGCACTTCTACCGCTCACTGCTGGAGACGATGACATGGGGGACCTGTGTGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704

Db 3061 GAGGAGTATCTGGTACCCCGAGCGGCTTCTTCTGTCCAGACCTTGGCCCCGGGCGCTGG 3120
QY 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGCTCCACCCACACAGGCACGCG 3144
RESULT 2
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Brickson
; APPLICANT: Ralph Schwalli
; APPLICANT: Mark Sliwowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-erbB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811.123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8
Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 57.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 9 Gaps: 1
US-09-493-480-7 (1-712) x US-09-811-123-8 (1-3768)
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Db 1 ATGGAGCTGGCGGCTTGTGCGCTGGGGGCTCTCTCCCTGCGCCCTCTTGGCCCCCGGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAGTGTGACCGGCGACACATGAGCTGGGCTCCCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACCTGGACATGCTCCGCGACCTCTACAGGGCTGCCAGCTGGGCTCCCTGCCAGTCCCGAG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 181 GAATCTACCTACCTACCTGCCCAATGCGAGCTGCTCTTCTCGCAGATATCCAGGAGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATGCTCACACCAAGTGGAGGAGTCCCACTGCAGAGGCTGCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATGTGCGAGGACACCCAGCTCTTTGAGGACAACTATGCGCTGCGCGCTGTCTAGCAATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCGCTGAAACAATACCCCTCTGTACAGGGGCTCTCCAGAGGAGCTTGGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAGCCCTCACAGATCTTGTGAAGAGAGGGGTCTTGATTCAGGGAGAACCCAG 480

Qy	161	Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Leu	Asp	Ile	Phe	His	Leu	Val	Asn	Asn	Gln	Leu	Ala	180			
Db	481	CTT	TGCT	TACC	GAG	GAC	CA	CA	TTT	TGT	GAG	AG	CA	AT	CTT	TCA	CA	AG	AA	CA	CC	AG	CTGGCT	540		
Qy	181	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	His	Pro	Cys	Ser	Pro	Met	Cys	Leu	Val	200			
Db	541	CTC	AC	CTG	AT	GAT	A	GAC	CA	CA	CCG	CT	CT	CGG	CC	TGC	CA	CC	CC	TG	TT	CT	CCG	ATGTTAAG	600	
Qy	201	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys		220			
Db	601	GGCT	CC	CGCT	GC	CT	GGG	GAG	AG	TT	CT	GAG	AT	TGT	CAG	AG	CC	TG	AC	GG	CG	CA	CTGTCGT	660		
Qy	221	Ala	Gly	Gly	Cys	Ala	Arg	Cys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys		240				
Db	661	GCC	GGT	GGCT	TGT	GCC	CGCT	C	AGG	GG	CA	CT	GCC	CA	CT	GAC	TG	CT	GC	CA	TAT	GAG	CA	GTGT	720	
Qy	241	Ala	Ala	Gly	Cys	Thr	Gly	Pro	Leu	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	His	Ser	Phe	Asn	His	260			
Db	721	GCT	GCC	GGCT	G	CA	CGG	CC	CC	CA	AG	CA	CT	CT	G	CA	CT	G	CT	G	CC	T	CC	CA	CTTCAACCAC	780
Qy	261	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu		280			
Db	781	AGT	GG	CA	CT	CT	TGT	GAG	CT	G	CA	CT	G	CC	CA	CT	TAC	AA	CA	CAG	CA	CA	CTTTGAG	840		
Qy	281	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	Tyr	Thr	Phe	Gly	Val	As	Ser	Cys	Val	Thr	Ala	Cys	Pro	300			
Db	841	TCC	AT	G	CC	CA	TCC	CA	GGG	CGG	GT	TAC	ATT	TGG	CC	AG	CT	TGT	GTG	ACT	G	CT	GT	CTCC	900	
Qy	301	Tyr	Asn	Tyr	Leu	Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln		320			
Db	901	TAC	AA	CT	TAC	CTT	CT	CA	GG	AG	CT	G	GG	AT	CT	TG	CA	CC	CT	G	CC	CT	CT	CTGCTGTCC	960	
Qy	321	Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	Pro	Cys	Ala	Arg		340			
Db	961	GAG	GT	CA	CAG	CA	GAG	AT	G	GA	CA	CA	CGG	TGT	GAG	AA	G	TG	CA	AG	CG	CC	CTGTGCCCCGA	1020		
Qy	341	Val	Cys	Trp	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	360				
Db	1021	GTG	TG	TAT	TGT	CT	G	GGG	CA	TGG	AG	CA	CTT	TGG	AG	TGT	GAG	GG	CAG	ATT	ACC	AG	CTTGCCCAT	1080		
Qy	361	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Leu	Val	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser		380			
Db	1081	AT	CC	AG	GAG	TTT	TG	CT	G	CTG	CA	AG	AG	AT	CTT	TGG	GAG	CT	TG	CA	TT	CTG	CCG	GAGAGC	1140	
Qy	381	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Glu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe		400			
Db	1141	TTT	GAT	TGG	GAC	CC	CA	CG	CT	CA	CA	CT	G	CC	CG	CT	CC	CA	CG	CA	CG	CTTCCAA	1200			
Qy	401	Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	420				
Db	1201	GAG																								


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Db 2641 GGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCCGCGGTTCACC 2700
Qy 653 ----- 653
Db 2701 CACCAGATGATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAGGGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGANTGTGGCCAGATTCGGGAGTTGTGTCTGTAATTCCTCCGATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCAGCGCTTTTGGTCAATCAGAAATGAGGACTTGGGCCCCAGGTCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3061 GAGGATGATCTGGTACCCAGAGGGCTTCTTCTGTCCAGNCCCTGCCCCGGGCGCTGGG 3120
Qy 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGGTCCACACAGGACCGC 3144
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RESULT 3

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US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent NO. US2002003736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811.115
; CURRENT FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 9 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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Qy 1 MetGluLeuAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGCGCTGGGGGCTCTCTCTCGCCCTTGTGCCCGGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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Db 61 GCGAGCACCCAGTGTGTGCACCGGCACAGACATGAGAGCTGGCGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACTGGACATGTCTCCGCCACCTCTACACAGGCTGCGAGGTGTGTCAGGAAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAATCACTACCTACCTGCCCCCAATGCCAGCTGTCTCTTCTGCGAGGATATCCAGAGGTG 240
Qy 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATCGCTCACACCAAGTAGGAGGAGGTCCTCACTGCGAGGCTGCGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCTGCTGGCGTCTAGACAAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGGAACAATACCACTGTCACAGGGGCTCTCCCGAGGAGGCTGCGGAGGTG 420
Qy 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValValLeuLeuGlnArgAsnProGln 160
Db 421 CAGCTTCGAGGCTCACAGAGATCTTGAAAGAGAGGGTCTTGATCCAGCGGAAACCCCG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACCCAGGACAGCATTTTGTGGAAGGACATCTTCCACACAGAACCAACAGCTGG 540
Qy 181 LeuThrIleLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACTGATAGACACCAACCGCTCTCGGGGCTGCCCCCTGTCTCCGATGTGTAAAG 600
Qy 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGAGTTGTACAGGCTGACCGGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCGGTGTGCTGTGCCCCGTGCAAGGGGCCACTGCCCCACTGACTGCTGCTGCATGAGCAGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCCGCTGCACGGGCCCCCAAGCACTCTGACTGCTGCTGGCTGCTCCACTTCAACCA 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCATGCCCCAGCCCTGTGCTACCTACACACAGACACGTTTGA 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCGAGGGCGGCTATACATTCGCGCGCCAGCTGTGTGACTGCTGTGCC 900
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisGlnGln 320
Db 901 TACAACCTACCTTCTACGGAGCTGGGATCTTCGACCCCTCGTCTGCTGCCCTTGCAACCA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACAGCAGAGGATGGNACACAGCGGTGTGAGAGTGCAGCAACCCCTGTGCCGA 1020
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaLen 360
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Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGGTGTGCTGCTGCAAGAGATCTTTTGGAGGCTGGGCAATTTCTGCCCGAGAG 1140
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; PRIOR APPLICATION NUMBER: US 09/493,480
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: US 60/117,976
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3768)
 ; OTHER INFORMATION: human HER-2/neu protein
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(1959)
 ; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2026)..(3765)
 ; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2968)..(3144)
 ; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
 ; NAME/KEY: misc feature
 ; LOCATION: (2968)..(3144)
 ; OTHER INFORMATION: preferred portion of the phosphorylation domain
 ; OTHER INFORMATION: (delta PD) of human HER-2/neu
 ; US-09-854-356-9

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 9 Gaps: 1

US-09-493-480-7 (1-712) x US-09-854-356-9 (1-3768)

QY	1	MetGluLeuAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuProGlyVala	20
DB	1	ATGGAGCTGGCGGCTTGTGCGCGCTGCGGCTCTCTCTCGCCCTCTTGGCCCGCGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GCAGGACCCAGTGTGCACCGGCACAGACATGAGCTGGGGCTCCCTGCGCATCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	121	ACCACCTGCACATGCTCCGCCACCTCTACCGAGGCTGCCAGGTGGTGCAGGGAACCTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
DB	181	GAACCTACCTTACCTGGCCCAATATGCGAGCTGTGCTTCTGCGAGGATATCCAGGAGGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTACGTGCTCATGGCTCACACCAAGTGCAGGAGGTCCCACTGCAGAGGCTGCGG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATATGCTGCGCGCTGTGTAGCAATGGA	360
QY	121	AspProLeuAsnAsnThrProValThrGlyAlaSerProGlyLeuArgGluLeu	140
DB	361	GACCCCTGAACAATATACACCCCTGTACAGGGGCTTCCCGAGAGGCTTGGCGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTTACAGAGATCTTGAAAGAGGGGTCTTGATCCAGCGGACCCCGAG	480
QY	161	LeuCysTyrGlnAspThrIleLeuTyrPheAspIlePheHisLysAsnGlnLeuAla	180

DB	481	CTCTGTACCAGGACACGATTTTGTGAAGGACATCTTCCACAAGAAACAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTTCCGATGTGAAG	600
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCGCTGCTGGGAGAGATTCTGAGGATTGTGAGAGCTTCAAGCGCACTGTCTGT	660
QY	221	AlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
DB	661	GCCGGTGGCTGTGCCCTCCAAAGGGGCCACTGCCCCACTGACTCTGCTGCATGAGAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGCTGCACGGGCCCCNAGCACTCTGACTGCTTGGCTTCCCTTCAACCCAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrArgThrPheGlu	280
DB	781	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTTACAACACAGACACGTTTGA	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCGAGGGCGGGTATACATTTGGCGCCAGCTGTGTGACTGCTTCCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACCTTCTACGGAGCTGGGATCTGCACCCCTGTCTGCCCTTGCACAAACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGGTGACAGCAGAGGATGAAACACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCC	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTGCTATGCTTGGGCATGAGGACCTTGCAGAGGTGAGGGAGGTGTACAGTGCCCA	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCAGAGGTTTGTGCTGCAAGAGATCTTTGGGAGCTTGGCATTTCTGCCGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1141	TTTGTATGGGACCCAGCTCCAACTCCCGCTCCAGCTCCAGCCAGAGAGCTCCAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
DB	1201	GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGAGCAGCTTGC	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCGTCTTCCAGAACCTTGCAGTAACTCCGGGAGCGAATTTCTGCACATGGG	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTTCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCTCATGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGGAGTGGATGCGCCCTCATCCACATTAACACCCACCTCTCTCTTGTGTGACACG	1440
QY	481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCGAGCTCTTTCGGAACCCGACCAAGCTCTGTCTCCACACTTGCACACG	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACGAGTGTGGCGGAGGGCTTGGCCCTGCCACCCAGCTGTGGCGCCGAGGAGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGGTCCAGGGGCCACCCAGTGTGTCAACTGACAGCGAGTTCTTCTTCGGGGCCAGG	1620

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Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAargHisCys 560
Db 1621 GTGAGGAATGCGAGTACTGCGGGCTCCAGGGCTCCAGGAGTATGTGAATGCCAGGCACGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGGCGTCCACCCCTGAGTGTGAGGCTCAGCCAGAAATGGCTCAGTGACCTGTTTGGACGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaAargCys 600
Db 1741 GCTGACCAAGTGTGGCTGTGGCCCTATAGGACCTTCCCTTCTGCTGGTGGCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGGAACCTGACCTCTCTACATGATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspHisLys 640
Db 1861 GGCGCATGCCAGCTTGGCCCATCAACTGACCCACTCTGTGTGGACCTGGATGACAAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GGTCTCCCGCCGACGAGAGAGCCAGCCCTCTGACGTCCATCTCTCGGTGGTGGC 1980
Qy 653 653
Db 1981 ATTCTGCTGCTGCTGTGGTCTTGGGGGTGGTCTTTTGGGATCTCTCATCAAGCGCGCAGCAG 2040
Qy 653 653
Db 2041 AAGATCCGGAAGTACACGATGCGGAGTCTGTCAGGAACCGAGTGTGTGGAGCGGTG 2100
Qy 653 653
Db 2101 ACACCTAGCGGAGCGATGCCAACCGGCGCAGATCGCGATCTGTAAAGAGACGGAGCTG 2160
Qy 653 653
Db 2161 AGGAAGTGAAGGTCTTGGATCTGGCGCTTTTGGCAGTCTACAAGGGCATCTGGATC 2220
Qy 653 653
Db 2221 CCTGATGGGAGATGTGAATAATCCAGTGGCCATCAAAAGTGTGTGAGGAAACACATCC 2280
Qy 653 653
Db 2281 CCCAAGCCCAACAAGAAATCTTAGACGAGCATAGTGTGCTGTGGTGGCTCCCA 2340
Qy 653 653
Db 2341 TATGTCTCCGCTTCTGGGCATCTGCTGACATCCACGTCAGCTGTGTGACACAGCTT 2400
Qy 653 653
Db 2401 ATGCCCTATGGTGCCTCTTAGACCATGTCCGGGAAAAACGGGAGCGCTGGGCTCCAG 2460
Qy 653 653
Db 2461 GACCTGCTGAATGGTGTATGACAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCG 2520
Qy 653 653
Db 2521 CTGCTACACAGGACCTTGGCGCTCGGAAGTGTGCTGTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 653
Db 2581 ATTACAGACTTGGGCTGGCTGGCTGGTGTGGAATTTGAAGAGACAGAGTACCATGAGAT 2640
Qy 653 653
Db 2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCCGCGGGCGTTCCNC 2700
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Qy 653 653
Db 2701 CACCAGAGTGTGTGTGGAGTTAAGTGTGACTGTGTGGAGAGCTGATGACTTTTGGGGCC 2760
Qy 653 653
Db 2761 AAACCTTAGATGGATCCAGCCCGGAGATCCCTGACCTGCTGAAAAAGGGGAGCG 2820
Qy 653 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATCTGATCATGTCTACATGATCATGTGCAATGTTGGATG 2880
Qy 653 653
Db 2881 ATTGACTCTGAATGTGGGCCAAGATTCCGGAGTGTGTCTGAAATCTCCCGCATGGCC 2940
Qy 654 654
Db 2941 AGGAGCCCCCAGCGCTTGTGTGTATCCAGATGAGGACTTGGCCCGCAGCATGCTCCCTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGTGGAGGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTGTATCCCGCAGCGGCTTCTTCTGTCCAGACCTTCCCGCGGCTGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGGTCCACACAGGCGCCGC 3144
RESULT 5
US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-930-125-1
Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 9 Gaps: 1
US-09-493-480-7 (1-712) x US-09-930-125-1 (1-3768)
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Db 1 ATGAGAGTGGCGCTTGTGGCGCTGCGGCTCTCTCTCGCCCTCTTGTGCCCCCGGAGCC 60
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Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	61	GCGAGCACCCAAAGTGTGCACCGGCACACATGAAGCTGGCGTCCCTGCCAGTCCCGAG	120
Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
Db	121	ACCCACCTGGACATGCTCCGCGCACTCTACAGGGCTGCCAGGTGGTGTGCAGGGAAACCTG	180
Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	181	GAATCACTACCTGCCCCACCAATGCCAGCTGTCTCTCTGCAGAGATATCCAGAGGTG	240
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTACGTGCTCATCGCTCAACAACAGTGAGCAGGTCCCACTGCAGAGGCTCGG	300
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	301	ATTGTGGGAGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCGCTGTGTAGACATGGA	360
Qy	121	AspProLeuAsnAsnThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	361	GACCCGCTGAACAATACACCCCTGTGCAGGGGCTCCCCAGAGAGGCTGCGGGAGCTG	420
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAGGCTCACAGAGATCTTGAAGGAGGGTCTTGATCCAGCGGAACCCCGAG	480
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGCTACCAGGACACGATTTGTGGAAGGACATCTTCCACAAGAACCAACCACTGGCT	540
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACACAACCGCTCTCGGGCCCTGCCACCCCTGTCTCCGATGTGTAAAG	600
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATTTGTGAGGCTTGACGGCCACTGTCTGT	660
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	661	GCCGCTGGCTGTGCGCGCTGCAAGGGGCCACTGCCCCACTGACTGCTGCCATGAGCAGTGT	720
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GCTGCCCGCTGCACGGGCCCCAAGCACTCTGACTGCTGGCTGGCTGCCCTCCACTTCAACCCAC	780
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTGAGCTGCATCTGCCAGCCCTGTGTCACTACACACAGACACGCTTTGAG	840
Qy	281	SerMetProAsnProGluArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCCGAGGGCCGGTATACATTTCCGCGCCAGCTGTGTGACTGCTGTGCC	900
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACCTACCTTTCTAGCGAGCTGGGATCTCTGCACCCCTCGTCTGCCCTCTGCACACCA	960
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	961	GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCACAAGCCCTGTGCCCGGA	1020
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1021	GTGTGCTATGCTGTGGGCATGGAGCACTTGGAGAGGTGAGGGCAGTTACCACTGCCAAT	1080
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGAGATTGTGCTGCTGCAAGAAATCTTTGGAGGCTTGGCAATTTCTGCCCGAGAGC	1140

QY	381	Phe	Asp	Gly	Asp	Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	400																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1141	TTT	GAT	GGG	ACC	CAG	CTC	CAA	CAC	TGC	CCG	CTC	CAG	CGC	CAG	CAG	CAG	CAG	CAG	CTC	CAAGTGT	1200																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	401	Glu	Thr	Leu	Glu	Glu	Leu	Thr	Gly	Val	Leu	Tyr	Leu	Tyr	Leu	Ser	Ala	Trp	Pro	Asp	Ser	Leu	Pro	420																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
DB	1201	GAG	ACT	CTT	GGA	GAG	ATG	TCA	CAG	GTT	TAC	CTT	TAC	ATC	TCT	CAG	CAT	TGC	CGG	ACG	CCT	GCCT	1260																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	421	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Leu	Arg	Gly	Arg	Gly	Leu	His	Asn	Gly	Val	Ala	440																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
DB	1261	GAC	CTC	AGC	GT	CTT	C	AGA	ACC	TGC	AA	GTT	TA	TCC	GGG	ACG	AA	TTC	TGC	ACA	AT	TGG	CGCC	1320																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
QY	441	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	Gly	Val	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Ser	Glu	460																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
DB	1321	TACT	CGCT	CA	CCCT	TGC	AA	GCG	CT	GGG	CAT	CAG	CT	TGG	CTG	GGG	CT	TGC	GT	GG	CT	1380																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	461	Leu	Gly	Ser	Gly	Leu	Ala	Leu	Leu	Leu	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	480																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
DB	1381	CTG	GGC	AGT	GG	ACT	TGG	CCC	CT	CA	TCC	ACC	TA	ACA	CCC	CAC	CT	CT	TGC	T	TC	GT	1440																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	481	Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	Ala	Asn	Arg	Pro	500																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1441	CCC	TGG	AGC	CAG	CT	TTT	T	CGA	ACC	CCG	CA	CA	AG	CT	CT	GC	T	CA	CAC	CT	GC	1500																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	501	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	520																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1501	GAG	CAC	GAG	TGT	TGG	GC	GAG	GGC	CT	TGG	CT	GCC	ACC	CAG	CT	TGT	GGC	CCG	AGG	GCA	CTGC	1560																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	521	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	540																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1561	TGG	GGT	CC	AGG	CCC	AC	CA	AGT	TGT	CAA	CT	GCA	CC	CAG	TTC	CTT	CGG	GCC	AGG	AGTGC	1620																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	541	Val	Glu	Glu	Cys	Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Ala	Ala	Arg	His	Cys	560																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1621	GTG	GAG	GAA	TGCC	CAG	TACT	TGC	AGGG	GGCT	CCCC	CAGGG	AGT	ATG	TGA	ATG	TCC	AGG	GGC	ACT	TGT	1680																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	561	Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	Phe	Gly	Pro	Glu	580																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1681	TTG	CGT	GCC	CAC	CC	TGAG	TGT	CAG	CCC	ACA	TGG	CT	CAG	TGAC	TGT	TTT	TGG	ACC	GGAG	1740																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
QY	581	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Leu	Asp	Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	600																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1741	GCT	GAC	CAG	TGT	TGG	CTG	TGG	CCC	ACT	AT	AAG	ACC	CTC	CT	CT	TCT	CGT	TGG	CCG	CTGC	1800																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	601	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	620																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1801	CCC	AG	CGT	GTG	AA	ACC	TGAC	CT	CT	CA	TGCC	CA	TCT	TGG	AAG	TTC	CAG	AT	GAGGAG	1860																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
QY	621	Gly	Ala	Cys	Gln	Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	640																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1861	GGC	GAT	GCC	CAG	CTT	GC	CC	CAT	C	ACT	GCA	CCC	ACT	CT	CT	TGT	TGG	AC	CTT	GAT	GACAAG	1920																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
QY	641	Gly	Cys	Pro	Ala	G	lu	Gln	Arg	Ala	Ser	Pro	Leu	Thr	Ser	-----	-----	-----	-----	-----	-----	653																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1921	GGCT	CCCC	CGC	GAC	GAG	AG	AG	CG	CC	CT	CT	GAC	GT	CC	CT	CT	CT	CG	GT	GG	1980																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	653	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	653																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	1981	ATT	CT	GCT	GGT	CTG	TGT	CTT	GGG	GGT	GGT	CT	TTT	GGG	AT	CT	CT	CA	AG	CG	AC	2040																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	653	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	653																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	2041	AAG	AT	CGG	AA	GT	AC	AG	TAC	AG	TAC	CGG	AG	CT	GCT	GC	AGG	AA	CGG	AG	CT	2100																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
QY	653	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	653																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	2101	AC	AC	TAG	CGG	AG	CG	AG	CG	CC	AA	C	AGG	CG	CAG	TG	CGG	AT	CT	CT	GAA	AG	AG	CGG	AG	CTG	2160																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
QY	653	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	653																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
DB	2161	AGG	AA	GGT	GA	AG	GT	CT	GT	GA	T	TT	GG	CA	AG	T	CT	T	T	T	T	GG	CA	AG	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT	GT	GA	T	CT

QY 261 SerGlyLeuCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTACCAACAGACAGACAGCTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 841 TCCATGCCCAATCCCGAGGCCGGTATACATTCCGGCCGACGCTGTGTGACTGCTGTCTCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACCTACCTTTCTACGACAGTGGGATCTCGACCCCTCGTCTGCCCTCGACCAACAA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGGATGAACACACGCGGTGTGAGAAGTGCAGAACCCCTGTGCCCCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGTCTGGGCATGGAGCACTTCCGAGAGTGGAGCGATTACAGTGCACAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGGAGTTTGTGCTGCCAAGAAGATCTTTGGGAGCCTGGCAATTTCTGCCGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1141 TTTGATGGGGACCCAGCCTCCACACCTGCCGCCCTCCAGCCAGAGCACTCCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAGAGATCAAGGTTTACCTATATCATCTCAGCATGGCCGAGACGCTGCCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGCTCTTCCAGAACCTTGCAGTAATCCGGGAGCAATTTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGCTCAGCTAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGACTGGCCCTCTCCACCATTAACCCACCTCTGCTTGTGTGCACACGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGGACCCAGCTCTTTCCGAAACCCGCCACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGGCGAGGGCCTGGCCTGCCACCCAGCTGTGCCGCCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCCAACCCAGTGTGTCACTGCAGCCAGTTCTTCCGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGATGCCAGTACTGCCAGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCCGTGCCACCCCTGAGTGTCCAGCCCAAGATGGCTCAGTGACCTGTGTTTGGACCGGAG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1741 GCTGACAGTGTGGCTGTGCCACTATPAGGACCTCCCTCTCTGCGTGGCCCGCTGC 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
DB 1801 CCCAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640

DB 1861 GGCGCATGCCAGCTTGGCCCATCACTGACACCCACTCTCTGTGTGGACTTGGATGCAAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 1921 GGCTGCCCGCCGAGCAGAGAGAGCCCTCTGACGTCCTCATCGTCTCTGCGGTGTGGC 1980
QY 653 ----- 653
DB 1981 ATTTCTGCTGCTGCTGTCTTTGGGGTGGTCTTTTGGGATCTCTCATCAAGCGAGCGGAGCAG 2040
QY 653 ----- 653
DB 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGAGAGCTGTTGGAGCCGCTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGGCGAGATGCCAACCCAGCGCGAGATGCGGATCTCTGMAAGAGAGCGAGCTG 2160
QY 653 ----- 653
DB 2161 AGCAAGGTGAAGTGTCTTGGATCTTGGGCTTTTGGGCAAGTCTCAAGGGCATCTGGATC 2220
QY 653 ----- 653
DB 2221 CCTGATGGGGAGAAATGTGAATAATTCAGTGGCCATCAAAAGTGTTCAGGGGAAAAACATCC 2280
QY 653 ----- 653
DB 2281 CCCAAAGCCAAAGAAATCTTTAGACGAAGCATACGTGTGATGGTGTGGGTCTCCCA 2340
QY 653 ----- 653
DB 2341 TATGTCTCCCGCTTCTTGGGCATCTGCTGACATCCAGGTGCAGCTGTTGACACAGCTT 2400
QY 653 ----- 653
DB 2401 ATGCCCTATGGCTGCCCTCTTAGACCATGTCCGGGAAAAACCGCGGACGCTGGGCTCCAG 2460
QY 653 ----- 653
DB 2461 GACCTGTGAATCTGGTGTATGATGATTTGCCAAGGGGATGAGCTTACCTGGAGAGTGTGCGG 2520
QY 653 ----- 653
DB 2521 CTGTGACACAGGAGCTTTGGCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAA 2580
QY 653 ----- 653
DB 2581 ATTACAGACTTGGGGCTGGCTCGGCTGTGACATTTGACGAGACAGAGTACATGCAGAT 2640
QY 653 ----- 653
DB 2641 GGGGCAAGTGTGCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGGGGTTACCC 2700
QY 653 ----- 653
DB 2701 CACCAGAGTGTGTGTGGAGTTATGTGTGTGATCTGTGTGGAGAGTGAATGATTTTGGGGCC 2760
QY 653 ----- 653
DB 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAGGGGGAGCGG 2820
QY 653 ----- 653
DB 2821 CTGCCCCAGCCCCCATCTGCACCATGTATGTCTACATGATCATGTGTCAAAATGTTGATG 2880
QY 653 ----- 653
DB 2881 ATTGACTCTGAATGTTCGGCCAGATTCCTGGAGTGTGGTGTGTGAATTTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
|||||

Db 2941 AGGACCCCCAGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCGAGTCCCTTG 3000
 Qy 665 AppSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyValAspAla 684
 Db 3001 GACAGCACCTTCTACCGCTCTACTGCTGAGGAGCATGACATGGGGACCTTGTGGATGCT 3060
 Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
 Db 3061 GAGGAGTATCTGTATCCCGCAGCAGCGCTTCTTCTGTCCAGACCTTGGCCCCGCGCGCTGGG 3120
 Qy 705 GlyMetValHisHisArgHisArg 712
 Db 3121 GGCATGGTCCACACAGGACCGC 3144

RESULT 7

US-10-280-576-3
 ; Sequence 3, Application US/10280576
 ; Publication No. US20040044405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wolff, Matthew R.
 ; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
 ; FILE REFERENCE: 09820.189
 ; CURRENT APPLICATION NUMBER: US/10/280,576
 ; CURRENT FILING DATE: 2002-10-22
 ; PRIOR APPLICATION NUMBER: 60/343,732
 ; PRIOR FILING DATE: 2001-10-25
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-280-576-3

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 13 Gaps: 1

US-09-493-480-7 (1-712) x US-10-280-576-3 (1-3768)

Qy 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
 Db 1 ATGGAGTGGCGGCTTGTGGCGCTGGGGCTCTCTGCGCTCTTGGCCCCCGAGGC 60
 Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 Db 61 GCGAGCACCAAGTGTGCACCGSCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 120
 Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 Db 121 ACCACCTGGATGCTCCGCCACCTCTACAGGGCTGCGAGTGTGCGGGAACCTG 180
 Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 Db 181 GAACCTACCTACCTGCCACCAATGCGAGCTGCTCTCTGCGAGTATCCAGGAGGTG 240
 Qy 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
 Db 241 CAGGGCTAGCTGCTATCGCTCACACCAAGTGGAGCGAGTCCCACTGCGAGAGGCTGCGG 300
 Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCGCTTGGCCCTGGCTGTAGCAATGGA 360
 Qy 121 AspProLeuAsnAsnThrThrProValThrGlyValAsaSerProGlyGlyLeuArgGluLeu 140
 Db 361 GACCCGCTGACATACCAACCCCTGTACAGGGGCTCCCGAGGAGGCTGCGGAGCTG 420
 Qy 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuGlnArgAsnProGln 160

Db 421 CAGCTTCGAGGCCCTCACAGAGATCTTGAAGAGGGGCTTCTGATTCAGCGGGAACCCCGAG 480
 Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
 Db 481 CTCTGCTACAGGACACGANTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 540
 Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 Db 541 CTCACATGATGAGACACCAACCGCTCTCGGGCTCCCAACCCCTGTTCTCCGATGTGTAG 600
 Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 Db 601 GECTCCCGCTGCTGGGAGAGATTCTGAGGATTTGTGAGAGCTTCAGAGCTTCACGGCCTGCTGT 660
 Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
 Db 661 GCGGTGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCCTCCACTTCAACCCAC 720
 Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 Db 721 GCTGCGGCTGCAAGGGGCCCAAGCACTCTGACTGCTGCTGCCCTGCCCTCCACTTCAACCCAC 780
 Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 Db 781 AGTGGCATCTGTGAGCTGCACTGCCCGCCCTGGTCACTTACCAACACACACAGCTTTGAG 840
 Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
 Db 841 TCCATGCCCATCCCGAGGGCGGTATACATTCGGGGCCAGCTGTGTGCTGCTGCTCCC 900
 Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
 Db 901 TACAACCTACTTCTACGAGCTGGGATCTGACACCTCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 Db 961 GAGGTGACAGCAGAGATGGAACACAGCGTGTGAGAGTGTGAGAGGCTTGTGCGGAGGC 1020
 Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 Db 1021 GTGTGCTATGCTTGGGCATGAGCACTTTCGAGAGGTGAGGGCAGTTTACCAGTGCAT 1080
 Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 Db 1081 ATCCAGAGTTTGTGCTGCTGCTGCAAGAGATCTTTGGAGGCTTGGCATTTCTGCGGAGAGC 1140
 Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnValPhe 400
 Db 1141 TTTGATGGGACCCAGCTTCAACACTGCCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 1200
 Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaIleProAspSerLeuPro 420
 Db 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGGCGGAGCAGCTGCT 1260
 Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
 Db 1261 GACCTCAGGCTTTCAGAACCTGCAAGTAATCCGGGAGCAATTCGCAATATGGCGCC 1320
 Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuArgSerLeuArgGlu 460
 Db 1321 TACTGCTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTGAGGGAA 1380
 Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
 Db 1381 CTGGGCACTGGAGCTGGCCCTCATCCACCATTAACCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 Db 1441 CCTTGGGACAGCTCTTTCGGAACCCGACCAAGCTCTGCTCCACACTGCTGCTGCTGCTGCTGCT 1500
 Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520

Db 1501 GAGGACGAGTGTGGCGAGGCGCTGGCTGCGCACGAGCTGTGCGCCCGAGGCGACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGGTCCAGGGCCACCCAGTGTGTCACTGAGCGAGTTCCTTTGGGGCGCAGGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTrpValAlaAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCGAGTACTGCGAGGGCTCCCGAGGGAGTATGTGAATGCGAGGCACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTCCCGTGGCCACCTGAGTGTGAGCCCGCCAGAAATGGCTCAGTACCTGTTTGTGACCGGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1741 GCTGACCAAGTGTGGCTGTGCGCCACTATAAGAGCCCTCCCTTCTGCGTGGCCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GGGCGATGCCGCTTGGCCCATCACTGACCCACCTCTCTGTGTGAGACCTGGATGACAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GGCTGCCCGCGAGCAGAGCCAGCCCTCTGAGGTCCATCTGCGGTGGTTGGC 1980
Qy 653 653
Db 1981 ATTCTGCTGCTGCTGTGGGTGTGGGTCTTTTGGGATCTCATCAAGCGACGCGAGCAG 2040
Qy 653 653
Db 2041 AAGATCCGGAAGTACAGATGCGGAGACTCTCTGAGGAAACGAGCTGTGGAGCCGCTG 2100
Qy 653 653
Db 2101 ACACCTAGCGGAGGATGCCAACACAGCGCGAGATCGGATCCTGAAAGAGACGAGCTG 2160
Qy 653 653
Db 2161 AGGAAGTGAAGTGTCTGTGATCTGGCGCTTTTGGCACTCTACAGGGCATCTGGATC 2220
Qy 653 653
Db 2221 CCTGATGGGAGAAATGTGAAAAATTCAGTGGCCATCAAAGTGTGAGGGAAACACATCC 2280
Qy 653 653
Db 2281 CCCAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGTGTGGGCTCCCA 2340
Qy 653 653
Db 2341 TATGTCTCCGCTCTCTGGGCATCTGCTTGACATCCACGGTGCAGCTGTGACACAGCTT 2400
Qy 653 653
Db 2401 ATGCCCTATGGCTCTCTTAGACCATGTCCGGGAAACCGCGGAGCGCTGGGCTCCAG 2460
Qy 653 653
Db 2461 GACCTGTGAACCTGGTGTATGACAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG 2520
Qy 653 653
Db 2521 CTGCTACACAGGACTTGGCGCTGCGAAGCTGTGTCAAGAGTCCCAACCATGTCAAA 2580
Qy 653 653
Db 2581 ATTACAGACTTGGGCTGGCTCGGCTGTGGAATTTGACGAGACAGAGTACCATGACAGAT 2640

Qy 653 653
Db 2641 GGGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAATCCATTCTCCGCGCGGGTTCACC 2700
Qy 653 653
Db 2701 CACCAGAGTATGTGTGGAGTTATGTGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 653
Db 2761 AAACCTTACGATGGATCCCGAGCCCGGAGATCCTTGACCTGTGGAAGAGGGGAGCGG 2820
Qy 653 653
Db 2821 CTGCCCCAGCCCCCATCTGACCATTTGATGTCTACATGATCATGTGTCAAATTTGGATG 2880
Qy 653 653
Db 2881 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCGATGCGC 2940
Qy 654 654
Db 2941 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGATCAGGACTTTGGGCCCGAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTrpLeuValProGlnGlnGlyPheCysProAspProAlaProGlyValaGly 704
Db 3061 GAGAGTATCTGTGTACCCCGAGCGGCTTCTTGTTCAGACCTTGCCCCCGGCGCTGGG 3120
Qy 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGCTCCACACAGCGCACCGC 3144

RESULT 8

US-09-765-973-1
; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 13 Gaps: 1

US-09-493-480-7 (1-712) x US-09-765-973-1 (1-3768)

Qy 1 MetGluLeuAlaIleLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGAGCTGGCGGCTTGTGCCCGCTGGGGCTCTCTCTGCGCCCTTGTGCCCGGAGCC 60

Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GGGAGCAACCAAGTGTGCACCGGCACACAGATGAAGCTGGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGCTCCGCCACCTCTACACAGGGCTGCACAGGTGGTGCAGGAAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACCTCACCCTACCTGCCACCAATGCCAGCCCTGTCTCTCTGCAGATATCCAGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTCTCATCGCTCACAAACCAAGTGAGCGAGGTCCCACTGCAGAGGCTGGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCAACCGAGCTCTTTGAGGACAACTATGCTTGGCCGTGTGTAGCAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAAACAATACCAACCCCTGTACAGGGGCTCCCAAGAGGCTGCGGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAGGCTCACAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACAGGACACGATTTGTGGAAGGACATCTTCCACAGAACAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACCAACCGCTCTCGGGCTGCCCCCTGTCTCCGATGTGAAG 500
Qy 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GACTCCCGCTGTGGGAGAGAGTCTTGAGGATTTGTACAGAGCTGACGGCGACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 661 GCGCGTGGCTGTGCCGCTGCAGAGGGGCCACTGCCCACTGACTGCTGCCATGACGAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGCTGCACGGGGCCCCAAGCACTCTGACTGCTTGGCTGGCTTCCACTTCAACCCAC 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACTGCCCGAGCCCTGTCACTACAAACACAGACAGCTTTGAG 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGGCGCCAGCTGTGTGACTGCTGTCCC 900
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACCTACTTTCTACGGAGCGTGGGATCTTGACCCCTGTGTGCTGCCCTTGCACACCAA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAGTGCAGAGCCCTGTGCCCGA 1020
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGGTCTGGGCAATGGAGCACTTTCGAGAGGTGAGGGCAGTTTACAGTGCCTAAT 1080
Qy 361 IleGlnGluPheAlaGlyCysLysValIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGAGTGTCTGGCTGCAAGAGATCTTTGGGAGGCTTGGCATTTCTGCCGGAGAGC 1140

Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGACCCAGCCTCCAAACATGCCCCGCTCCAGCCAGAGAGCTCCAAGTGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
Db 1201 GAGACTCTGGAAGAGATCACAGGTTCCTATACATCTCAGCATGCGCGACAGCTGCCT 1260
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1261 GACCTCAGCGCTCTTCAGAACCTGCAAGTAATCGGGACGAATTCGCAACAATGGCGC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGCTGACCTTCGAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGCTCAGTGAAGA 1380
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1381 CTGGGCACTGGAGTGGCCCTCATCCACCATACACCCACCTCTGCTTCGTGCACACGGTG 1440
Qy 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1441 CCTTGGGACCACTCTTTCGGAACCGCACCAAGCTCTGCTCCACACTGCACACCGGCCA 1500
Qy 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1501 GAGGACGAGTGTGGGGAGGGCTGGCTTCCACACGCTGTCGCCCGCGAGGGCACTGC 1560
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1561 TGGGTTCAGGGCCCAACCCAGTGTCTCACTGACGACAGTTCCTTGGGGCCAGGAGTGC 1620
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1621 GTGGAGGAATGCCAGTACTGACGGGCTCCCGAGGAGTATGTGAATGCACAGCACTGT 1680
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCGCGTGCACCCCTGAGTGTGAGCCCCAGAAATGGCTCAGTGACCTGTGTTTGACCCGAG 1740
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
Db 1741 GCTGACCACTGTGTGGCTGTGCCCACTATAGGACCTCTCCCTTCTCGGTGGCGCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GGGCGCATGCCAGCTTGGCCCCATCAATGTCACCTCTCTGTGTGGACCTGGATGACAG 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 1921 GACTGCCCGCGCAGGACGAGAGCGCAGCCCTCTGACCGTCCATCATCTCTCGGTGGTGGC 1980
Qy 653 653 653 653
Db 1981 ATTCTGCTGTGTGGTCTTGGGGTGGTCTTTGGGATCTCTCATCAGCGACCGCAGCAG 2040
Qy 653 653 653 653
Db 2041 AAGATCCGGAAGTACACGATGCGAGACTGCTGCAGGAACCGGAGCTGTGTGGAGCCGCTG 2100
Qy 653 653 653 653
Db 2101 ACACCTAGCGGACGATGCCCAACCGAGCGCAGATGGGATCTCTGAAGAGAGACGAGCTG 2160
Qy 653 653 653 653
Db 2161 AGGAAGTGAAGGTGTGGATCTGGCGCTTTTGGCACAGTCTTACAAGGCACTCTGGATC 2220
Qy 653 653 653 653

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Db 2221 CCTGATGGGAGAAATGTGAAAATTCAGTGGCCATCAAGTGTGAGGGAAAAACACATCC 2280
Qy 653 -----
Db 2281 CCCAAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCCA 2340
Qy 653 -----
Db 2341 TATGTCTCCCGCTCTCTGGGCAATCTGCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2400
Qy 653 -----
Db 2401 ATGCCCTATGGCTGCTCTTAGACCATGCTCCGGGAAAAACCGGACGCTGGGCTCCAG 2460
Qy 653 -----
Db 2461 GACCTGTGAACCTGTGTATGCAATGTCAGAGGATGAGCTACCTGGAGGATGTGGG 2520
Qy 653 -----
Db 2521 CTCTACACAGGACTTGGCGGCTCGGAAGTGTCTGCTCAAGTGTCCCAACCATGTCAA 2580
Qy 653 -----
Db 2581 ATTACAGACTTGGGCTGGCTCGGCTGTGACATTTGACGAGACAGATACCATGCAGAT 2640
Qy 653 -----
Db 2641 GGGGCAAGTGGCCCATCAAGATGATGGCTGGAGTCCATTTCTCCCGCGCGTTCCAC 2700
Qy 653 -----
Db 2701 CACCAGATGATGTGTGGATTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 -----
Db 2761 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGGGGGAGCGG 2820
Qy 653 -----
Db 2821 CTGCCCCAGCCCCCATCTGCACCATGATGTCTACATGATCATGGTCAATGTGGATG 2880
Qy 653 -----
Db 2881 ATTGACTCTGAATGTCCGCCAAGATTCCGGAGTGGTGTCTGAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGACCCCCAGCGCTTTGTGTCATCCAGAAATGAGGACTTGGGCCCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACTTTCTACCGCTCACTGTGGAGACCATGATGATGGGGGAGCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyValaGly 704
Db 3061 GAGAGTATCTGGTACCCACAGCAGGGCTTCTCTGTCCAGACCTTGCCCCGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCGATGTCCACACAGGACCGC 3144
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RESULT 9

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US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
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; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
; US-10-313-644-1
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1
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US-09-493-480-7 (1-712) x US-10-313-644-1 (1-3768)

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Qy 1 MetGluLeuAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTTGTCCGCTGGGGCTCTCTCGCCCTTTGCCCTTTCGCCCGGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGACCGGCACAGACATGAGCTGGCGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACCTGGACATGCTCGCCACCTCTTACAGGGCTGCCAGGTGGTGCAGGGAAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAATCTACCTACCTACCTGCCCAATGCCAGCTGCTCTTCTCCAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATGCTCACAACCAAGTAGAGAGGTCCCACTGCAGAGGCTGCGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGGAGGACCCAGCTCTTTGAGGACAATATGCTCCCTGGCCGTGTACACAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCTCCAGGAGGCTTCCGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAACCTCAGAGATCTTGAAGAGAGGGGTCTTGATCCAGCGGAAACCCCAAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACACAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAG 600
Qy 201 GlySerArgCysTyrGlyLeuSerSerGluSerCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGAGAGATTTCTGAGGATTTCTAGAGCTTACAGCGGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCCGGTGGCTGTGCCCGCTGCAGAGGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Db	721	GCTGCGGCTGCACGGGCCCCAAGCACTCTGACTGCTGGCTGCTCCACTTCAACCCAC	780	Db	1801	CCCAGCGGTGTAACCTGACCTCTCTACATGCCCATCTGGAGTTTCCAGATGAGGAG	1860
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	781	AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACCTCAACACACAGACACGTTTGAG	840	Db	1861	GGCGCATGCCAGCTTTGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG	1920
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	841	TCCATGCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTCC	900	Db	1921	GGCTGCCCGCCGCGAGAGAGACCGACCCCTCTGACGTCCATCATCTCTCGCGGTGGTTGGC	1980
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Qy	653	-----	653
Db	901	TACAACTACCTTTCTACGAGCTGGATCTCTGACCTCTGCTGCTGCCCTGCACACCAA	960	Db	1981	ATTCTGCTGCTCGTGGTCTTGGGGGTGGTCTTTTGGGATCCTCATCAAGCGACCGCAGCAG	2040
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Qy	653	-----	653
Db	961	GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCGA	1020	Db	2041	AGATCCCGAAGTACACGATGCGGAGACTGCTGCAGGAAACCGGAGCTGGTGGAGCGCTG	2100
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Qy	653	-----	653
Db	1021	GTGTCTATFGTCTGGGCTAGGACACTTGCAGAGGTGAGGGCAGTTACCACTGCCAAT	1080	Db	2101	ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGCGGATCCTGMAAGAGACGGAGCTG	2160
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Qy	653	-----	653
Db	1081	ATCCAGGAGTTTGTCTGGCTGCAGAAGATCTTTGGGAGCTGGCATTTCTGCCGGAGAGC	1140	Db	2161	AGGAAAGTGAAAGTGTGGATCTGGCGCTTTTGGGCACAGTCTACAAGGGCATCTGGATC	2220
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluLeuGlnValPhe	400	Qy	653	-----	653
Db	1141	TTTGTATGGGGACCCAGCCCTCCAACTATGCCCGCTCCAGCCAGAGAGCTTCAAGTGT	1200	Db	2221	CCTGATGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAGTGTGTGAGGGAAACACATCC	2280
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420	Qy	653	-----	653
Db	1201	GAGACTCTGGAAGAGATCACAGTTACCTATACATCTCAGATGGCCGACAGCCCTGCT	1260	Db	2281	CCCAAGCCCAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2340
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Qy	653	-----	653
Db	1261	GACCTCAGCGTCTTCAGAACTGCAAGTAATCCGGGGACGAATCTGCACAAATGGCGC	1320	Db	2341	TATGTCTCCCGCTTCTGGGCATCTGCCGATCCACGTCGACGTCGTGTGACACAGCTT	2400
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460	Qy	653	-----	653
Db	1321	TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGGCTCCTCCTGAGGAA	1380	Db	2401	ATGCCCTATGCTGCTCTTAGACCATGTTCGGGAAAAACGCGGACGCTTGGGCTCCAG	2460
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480	Qy	653	-----	653
Db	1381	CTGGGCGTGGACTGGCCCTCATCCACCATACACCCACTCTGCTTCTGTGCACACGGTG	1440	Db	2461	GACCTGCTGAATGCTGTGTATGAGATTGCAAGGGGATGAGCTACCTGGAGGATGTGGG	2520
Qy	481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	Qy	653	-----	653
Db	1441	CCCTGGGACCACTCTTCGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1500	Db	2521	CTCGTACACAGGACTTGGCCGCTCGGAACGTCGTGGTCAAGAGTCCCAACCATGTCAA	2580
Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Qy	653	-----	653
Db	1501	GAGGACAGTGTGTGGGGAGGGCCCTGGGCTGCGCACAGCTGTGGCCCGAGGGCACTGC	1560	Db	2581	ATTACAGACTTGGGCTGCTGGCTGGACATTTGACGAGACAGAGTACCATGCAAGAT	2640
Qy	521	TyrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Qy	653	-----	653
Db	1561	TGGGGTCCAGGGCCCAACCAAGTGTGTCACTGACGACCAAGTTCTTCCGGGCCAGGAGTGC	1620	Db	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTTCATTCTCCGCCGCGGTTCAAC	2700
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Qy	653	-----	653
Db	1621	GTGGAGGAATGCCAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1680	Db	2701	CACCAGATGATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2760
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	Qy	653	-----	653
Db	1681	TTGCCGTGCCCTCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTTTTGGACCGGAG	1740	Db	2761	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGGGGGAGCGG	2820
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	Qy	653	-----	653
Db	1741	GCTGACCAGTGTGGCTGTGCCACTATAAGGACCTTCCCTTCTCGGTGGCCCGCTGC	1800	Db	2821	CTGCCCGACCCCCATCTGACCAATGATGTCTACATGATCATGTGTCAAATGTGTGATG	2880
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620	Qy	653	-----	653
Db				Db	2881	ATTGACTCTGAATGTGGGCCAAGATTCGGGGAGTTGGTGTCTGAATTCCTCCGCAATGCC	2940


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Qy 654 -----GlnAenGluAepLeuGlyProAlaSerProLeu 664
Db 2941 AGGACCCCCAGCGCTTGTGGTCAATCAGAAATGAGGACTTGGGCCAGCCAGCTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAepAspMetGlyAspLeuValAepAla 684
Db 3001 GACAGCACTTCTACCGCTCACTGCTGGAGGACCATGACATGAGGGGACCTGGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCAGCAGGGCTTCTTCTGTCAGACCTTGCCCGGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGTGTCCACACAGGACCCGC 3144

RESULT 10
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US2003008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disiol, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 336
Query Match: 95.50% Indels: 1
DB: 10 Gaps: 1

US-09-493-480-7 (1-712) x US-09-441-411-5 (1-4473)
Qy 1 MetGluLeuAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCCTCTCGGCCCTTTGCCCGCCGAGCC 234
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCAGACCCCAAGTGTGCACGGCACAGATGAGCTGGCGCTCCCTGCCAGTCCCGAG 294
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCACTGGNACATGCTCCGCCACTCTACAGGGCTGCCAGGTGGTGAGGGAACCTG 354
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GNACTACCTACCTGCCCAACCAATGCCAGCGCTGCTTCTTCAGAGATATCCAGAGGTG 414
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTCGTCATGCTCACAACCAAGTGGAGGAGGTGCCACTGCAGAGGCTCGCG 474
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 475 ATTGTGGAGGACCCAGCTCTTTGAGGACCACTATGCCCCTGGCGGTGCTAGACAATGGA 534
Qy 121 AspProLeuAenAenThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140

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Db 535 GACCGCTGAACAATATACACCCCTGTCAAGGGGCTTCCCCAGAGGCTTCGGGGAGCTG 594
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAenProGln 160
Db 595 CAGCTTCGAGGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 654
Qy 161 LeuCysTyrGlnAepThrIleLeuTrpLysAspIlePheHisLysAenAenGlnLeuAla 180
Db 655 CTCTGCTACACGAGCACGATTTGTGGAAGGACATCTTCACAAGAACAACACGCTGGCT 714
Qy 181 LeuThrLeuIleAepThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTCTGCCACCTGTCTCCGATGTGTAG 774
Qy 201 GlySerArgCysTrpGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 775 GGCTCCCGCTGCTGGGGAGAGGTCTTCAGGAGTTGTACAGGCTTGACGGCGCATGTCTGT 834
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 835 GCGGTGCTGTGCGCGCTGCAAGGGGCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAenHis 260
Db 895 GCTGCGGCTGCACGGGCCCCCAAGCACTCTGACTGCTGGCTGGCTCCACTTCAACCCAC 954
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 955 AGTGCACTGTGAGCTGCACTGCCACGCCCTGGTCACTACACACACACAGCTTGAG 1014
Qy 281 SerMetProAenProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 1015 TCCATGCCCAATCCGAGGCGGTATACATTTGGCGGCGAGCTGTGTGAGCTGCTGTCCC 1074
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAenGln 320
Db 1075 TACAACCTACCTTTCTACGGAAGTGGATCTTGCACCTCTGCTGCTGCCCTTCGACAAACCA 1134
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1135 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAGAGTGCAGCAAGCCCTGTGCCCGA 1194
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAen 360
Db 1195 GTGTGCTATGCTTGGGCATGAGCACTTGCAGAGGTGAGGGCAGTTACACAGTGCAT 1254
Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1255 ATCAGGAGTTGTCTGGCTGCAAGAGATCTTTGGGAGCTTGGCATTTCTCCGGAGAGC 1314
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
Db 1315 TTTGATGGGACCCAGCTCCCACTGCCCGCTCCAGCCAGAGCAGCTCCAGTGTGT 1374
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1375 GAGACTCTGGAAGAGATCACAGGTTTACCTATACATCTCAGCATGCGCGACAGCTGCT 1434
Qy 421 AspLeuSerValPheGlnAenLeuGlnValIleArgGlyArgIleLeuHisAenGlyAla 440
Db 1435 GACTCAGCGTCTTCAGAACCTGCAAGTAAATCCGGGAGCGAATTTCTGCACATGTCGCC 1494
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1495 TACTGCTGACCTTGCAGAGGCTGGGCATAGCTGGCTGGGGCTGGGCTCACTGAGGAA 1554
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAenThrHisLeuCysPheValHisThrVal 480
Db 1555 CTGGGAGTGAGCTGGGCTCTCATCCACATAACACCCACTCTGCTGCTGTCACACGGTG 1614
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAenArgPro 500

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Db 1615 CCCTGGGACAGCTCTTTCCGGAACCGGACCAAGCTCTGCTCCACACTGCGCAACCGGCCA 1674
Qy 501 GluAspGluCysValGlyGluGluAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1675 GAGGACGAGTGTGTGGGGAGGGCTGGCCCTGCCACCAAGCTGTGGCCGAGGCGACTGC 1734
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGluGluCys 540
Db 1735 TGGGGTCCAGGGCCACCAGTGTGTCACTGCAAGCCAGTGTCTTGGGGGCCAGAGTGC 1794
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1795 GTGAGGAGATCCGAGTACTGCGAGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1854
Qy 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1855 TTGCGGTGCCACCTGTAGTGTGAGCCCGAGGCTATAGGAGCCCTCCCTTCTGGGTGGCCCGTGC 1914
Qy 581 AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProPheCysValAlaArgCys 600
Db 1915 GCTGACCAAGTGTGTGGCCCTGTGGCCACTATAGGAGCCCTCCCTTCTGGGTGGCCCGTGC 1974
Qy 601 ProSerGlyValIlyAspLeuSerTyrMetProIleTyrPhePheProAspGluGlu 620
Db 1975 CCCAGCGTGTGAACCTGACTCTCTTACATGCCCCATCTGGAAGTTTCCAGATGAGGAG 2034
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspIly 640
Db 2035 GGGCGATGCCAGCTTGGCCCATCACTCACTGACCCCACTCTCTGTGTGAGCTGTGATGACAAG 2094
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 2095 GGCTGCCCCCGGAGACAGAGCCAGCCCTCTGAGCTCATCATCTCTGCGGTGGTTGGC 2154
Qy 653 ----- 653
Db 2155 ATTCTGCTGTGTGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGAGCGGACGAG 2214
Qy 653 ----- 653
Db 2215 AAGATCCGGAAGTACACGATCGGAGACTGCTGTCAGGAAACGGAGCTGTGTGGAGCGGCTG 2274
Qy 653 ----- 653
Db 2275 ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGCGGATCTCTGAAGAGAGCGAGCTG 2334
Qy 653 ----- 653
Db 2335 AGGAAGTGAAGTGTGTGGATCTGGGCTTGGGCTTTTGGCACAGTCTACAGGGCATCTGGATC 2394
Qy 653 ----- 653
Db 2395 CCTGATGGGAGATGTGAATAATTCAGTGGCCATCAAAAGTGTGTGAGGGAACACATCC 2454
Qy 653 ----- 653
Db 2455 CCCAAGCCAAACAAAGAAATCTTAGACGAAGCATAGTATGGCTGGTGGGCTCCCA 2514
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Db 2515 TATGTCTCCGCTTCTGGGATCTGCTGATCCACGGTGCAGCTGTGTGACACAGCTT 2574
Qy 653 ----- 653
Db 2575 ATGCCCTATGGTGTCTTAGACCATGTCCGGGAAACCGCGGAGCGCTGGGCTCCAG 2634
Qy 653 ----- 653
Db 2635 GACCTGTGAACCTGTGTATGAGATTTGCAAGGGGATGAGCTACTGAGGAGATGTGGG 2694
Qy 653 ----- 653
Db 2695 CTCGTACACAGGAGCTTGGCCGCTCGGAACGTGTGCTGCTCAAGAGTCCCAACCATGTCAA 2754

Qy 653 ----- 653
Db 2755 ATTACAGACTTTCGGGCTGGCTGGCTGGCATTTGACGAGACAGAGTACCATGAGAT 2814
Qy 653 ----- 653
Db 2815 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGGTTTACC 2874
Qy 653 ----- 653
Db 2875 CACCAGAGTGAATGTGTGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
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Db 2935 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAGGGGAGCGG 2994
Qy 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCAACCATTTGATGTCTACATGATCATGTCAAATGTTGGATG 3054
Qy 653 ----- 653
Db 3055 ATTGACTCTGAATGTGGCCCAAGATTCCGGGAGTTGGTCTCTGAATTTCTCCGCGATGGCC 3114
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGACCCCCAGCGCTTTGGTGTATCCAGAAATGAGGACTTGGGCCACGCGCATCTCCTTG 3174
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3234
Qy 685 GluIlyTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTACTACCCAGCAGGGCTTCTTCTGTCCAGACCTGCCCCGGGCGCTGGG 3294
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3295 GGCATGTCTCCACACAGGCGCCGC 3318

RESULT 11
US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-7 (1-712) x US-10-146-473-32 (1-4473)

QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla 20
DB 175 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGCCCGGAGCC 234
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 235 GCAGCACCACCACTGTGTGACCGGCACAGACATGAAGCTGGGGCTCCCTGCGCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValValGlnGlyAsnLeu 60
DB 295 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 354
QY 61 GluLeuThrTyrglnProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 355 GAACCTCACCTACCTGCCACCAATGCCAGCTGTCTCTCTGAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrglnValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 415 CAGGGCTACGTGTCTCATCGCTCAACCAAGTGAAGTGGAGCTCCCACTGCAGAGGCTGGCG 474
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrglnAlaLeuAlaValLeuAspAsnGly 120
DB 475 ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACATGTCCTGCGCTGTGTAGCAATGGA 534
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 535 GACCCCTGAAACATACCACTCTGTGTCAGAGGGCTCCGCCAGAGGCTTCGGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 595 CAGCTTCGAAGCTTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG 654
QY 161 LeuCysTyrglnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 655 CTCTGTACAGGACACGATTTTGTGAAGGACATCTTCACAGGAACAACCACTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 715 CTCACTGATAGACACCAACCCCTCTCGGGCTTCGCCCTCTCTCTCGGATGTGTAG 774
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 775 GGCTCCCGCTGTGGGAGAGATCTCTGAGATTGTTCAGAGCTGCAGCGCTGTCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 835 GCGGTGGCTGTCCCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCTGCTGCTGCTG 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 895 GCTGCCGGCTGACCGGGCCCAAGCACTCTGACTGCCCTGGCCCTGCCCTTCACACCAC 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrglnAspThrPheGlu 280
DB 955 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGCTCACCTACACACAGACAGATTGAG 1014
QY 281 SerMetProAsnProGluGlyArgTyrglnThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 1015 TCCATGCCCAATCCCGAGGGCGGTATATACATTCGGGCCAGCTGTGTGACTGCTGTCCC 1074
QY 301 TyrAsnTyrglnSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1075 TACAACCTACCTTTCTACGGGAGTGGGATCTCGACCCCTGCTGCTGCCCTGCGACACACCA 1134
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 1135 GAGTGACAGCAGGAGATGGAACACAGCGGTGTGAGAGTGCAGAGGACCTGTGCGCGA 1194
QY 341 ValCysTyrglnGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360

DB 1195 GTGTGCTATGCTCTGGGCATGGAGCACTTGGAGAGGTGAGGGCAGTTACCAGTCCCAAT 1254
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1255 ATCCAGGAGTTTGTGCTGGCTGCAAGAGATCTTTGGGAGCCTGGCATTTCTGCGGAGAGC 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1315 TTTGATGGGAGCCAGCTCCAACTGCGCCCTCCAGCCAGAGAGCTCCAAGTGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrglnLeuTyrglnSerAlaTrpProAspSerLeuPro 420
DB 1375 GAGACTCTGGAAGAGATCAGAGTTACTATATATCTCAGCATGCGCCGACAGCTGTCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACTCAGCGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCAAGATTCTGCAATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1495 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1555 CTGGGAGTGGAGCTGGCCCTCATCCACCATTAACACCCACTCTCTCTGTCGACACAGGTG 1614
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1615 CCCTGGGACCAGCTCTTTCCGNAACCCGACCAAGCTCTGCTCCACACTGCCCAACCGGCA 1674
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1675 GAGGACGAGTGTGGGCGAGGGCTGGCCCTGCCACAGCTGTGCGCCGAGGGCAGCTGC 1734
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1735 TGGGGTCCAGGGGCCACCCAGTGTGTCACTGCGAGCCAGATTCTCTGGGGGCGAGAGTGC 1794
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGlyTyrglnValAsnAlaArgHisCys 560
DB 1795 GTGGAGGAATGCCGAGTACTGCGAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1854
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1855 TTGCGGTGCCACCTGAGTGTGTCAGCCCCAGAAATGGCTCAGTGACCTGTGTTTGGACCGAG 1914
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrglnAspProProPheCysValAlaArgCys 600
DB 1915 GCTGACAGTGTGTGGCTGTGGCCCTGTGGCCACTATAAGGACCCCTCCCTCTGCGTGGCCGCTGC 1974
QY 601 ProSerGlyValLysProAspLeuSerTyrglnMetProIleTrpLysPheProAspGluGlu 620
DB 1975 CCAGCGGTGTGAACCTGACCTCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2034
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2035 GGGCGCATGCCAGCTTGGCCCATCACTGCAACCACTCTCTGTGTGGAGCTCTGATGACAAG 2094
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 2095 GGCTGCCCCCGAGCAGAGAGCGCCCTGTGACGTCCATCATCTCTGCGGTGGTGGC 2154
QY 653 ----- 653
DB 2155 ATTCTGCTGTGCTGTCTTGGGGGTGGTCTTTGGGATCTCTCATCAAGCGGACGAGCAG 2214
QY 653 ----- 653
DB 2215 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCGGAAACGGAGCTGTTGGAGCCGCTG 2274
QY 653 ----- 653
DB 2275 ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATCGGATCTCTGAAAGAGACGAGGCTG 2334

QY	241	AlaAlaGlyCysThrGlyProIysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260		1975	CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGAG	2034
DB	895	GCTGCCGGCTGCACCGGCCCCAAGCACTCTGACTGCTGGCTGCTCTCCACTTCAACCCAC	954				
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280		621	GlyValaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	955	AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTTACCAACAGACACAGCTTTGAG	1014		2035	GGCGATGCCAGCTTGCCCCCACTCACTGACCCACTCTCTGTGTGGACTGTGATGACAAG	2094
QY	281	SerMetProAsnProGluAlaGlyArgTyrThrPheGlyValaSerCysValThrAlaCysPro	300		641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	1015	TCATGCCCCATCCGAGGCGCGGTATACATTGGCGCCAGCTGTGTGACTGCTGTGCC	1074		2095	GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCCATCATCTCTGCGGTGGTTGGC	2154
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320		653	-----	653
DB	1075	TACAACTACCTTTCTAGGAGGTGGATCTCTGCACCTGCTGCTGCCCTGCACCAACAA	1134		2155	ATTCTGCTGTCGTGTGTTTGGGGTGTCTTTTGGGATCTCTCATCAAGCGACGGCAGCAG	2214
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340		653	-----	653
DB	1135	GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCAGAGCCCTGTGCCGA	1194		2215	AAGATCGGAAGTACACGATGCGGAGACTGCTGCGAANAACGGAGCTGGTGGAGCGCGTG	2274
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360		653	-----	653
DB	1195	GTGTGCTATGTCTGGGCATGGAGCACTTCGAGAGGTGAGGGAGTTTACAGTGCCTAT	1254		2275	ACACCTAGCGGAGCGATGCCAACACAGCGCAGATGCGGATCTCTGAAAGACAGCGAGCTG	2334
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380		653	-----	653
DB	1255	ATCCAGGAGTTTGTGCTGTCAGAGAGATCTTTGGGAGCTTGCAATTTCTGCCGAGAGC	1314		2335	AGGAAGGTGAAGTGTGTGATCTGCGCTTTTGGGCACAGTCTTACAAGGGCATCTGGATC	2394
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400		653	-----	653
DB	1315	TTTGATGGGACCCAGCCTCCAACTGCGCCCTCCAGCCAGAGCAGCTCCAAGTGT	1374		2395	CCTGATGGGGAGAAATGTGAAAATTCAGTGGCCCATCAAGTGTGTGAGGGAACACATCC	2454
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420		653	-----	653
DB	1375	GAGACTCTGGAAGAGATCAAGGTATACCTATATATCTCAGCATGGCGGACAGCTGCCT	1434		2455	CCCAAGSCCAACAAAGAAATCTTAGACGAAGATACGTGATGCTGTGTGGCTCCCA	2514
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440		653	-----	653
DB	1435	GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACAATGGGCGC	1494		2515	TATGTCTCCGCTTCTGGGCATCTGCTGCATCCACGGTGCAGCTGGTGACACAGCTT	2574
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpIleuArgSerLeuArgGlu	460		653	-----	653
DB	1495	TACTCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTGAGGGA	1554		2575	ATGCCCTATGGCTGCCCTTTAGACCATGTTCGGGAAAACCGCGGACCGCTGGCTCCAG	2634
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480		653	-----	653
DB	1555	CTGGGAGTGGACTGGCCCTCATCCACATPACACCCACCTCTGCTTCTGTGCACAGGTG	1614		2635	GACCTGCTGAACCTGGTGTATATGCAGATGTCGAAGGGGATGAGCTACCTGGAGGATGTGCG	2694
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500		653	-----	653
DB	1615	CCCTGGGACCACTCTTTGGGACCCGACCAAGCTCTGCTCCACACTGCGCAACCGGCCA	1674		2695	CTCGTACACAGGACCTTGGCGCTCGGAACGTGCTGTGTGCTCAAGAGTCCCAACATGTCAA	2754
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520		653	-----	653
DB	1675	GAGGACAGGTGTGTGGCGGAGGCTGGCTGCTGCGCCAGCTGTGCGCCCGAGGCGCACTGC	1734		2755	ATTACAGACTTGGGCTGGCTGGCTGCTGACATTTGACGAGACAGAGTACCATGCAGAT	2814
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540		653	-----	653
DB	1735	TGGGTCGAGGCGCCACCCAGTGTGTCACTGACGACAGTTCCTTGGGGCGAGAGTGC	1794		2815	GGGGCAAGGTGCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCCGCGCGGTTCACC	2874
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560		653	-----	653
DB	1795	GTGGAGGAATGCCAGTACTGCAAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1854		2875	CACCAGATGATGTGTGGAGTTATGGTGTGATGTGTGTGGGAGCTGTGATCTTTTGGGGCC	2934
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580		653	-----	653
DB	1855	TTGCCGTGCCACCTGAGTGTGACCCCAAGTGGCTCAGTGACCTGTTTGTGACCGGAG	1914		2935	AAACCTTACGATGGGATCCCGCGGAGATCCCTGCACCTGTGGAAGAGGGGAGCGG	2994
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600		653	-----	653
DB	1915	GCTGACCAAGTGTGGCTGTGCCCCACTATAGGACCTCTCTCTGCGTGGCCCGCTGC	1974		2995	CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTTACATGATCATGTGTCAAAATGTTGGATG	3054
QY	601	ProSerGlyValLysProAspLeuSerTyrMetTrpLysPheProAspGluGlu	620		653	-----	653

Db 3055 ATTGACTCTGAATGTGGCCCAAGANTTCGGGAGTTGGTGTCTGAATTTCTCCGCGATGGCC 3114
 Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
 Db 3115 AGGACCCCGCCAGCGCTTTGTGTCTCATCCAGATGAGGACTTGGGCCCGCCAGCTCCCTTG 3174
 Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
 Db 3175 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAGCTGTGTGGATGCT 3234
 Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
 Db 3235 GAGGAGTATCTGGTACCCCGAGCGGCTTCTCTGTCCAGACCCCTGCCCCGGGCGCTGGG 3294
 Qy 705 GlyMetValHisHisArgHisArg 712
 Db 3295 GGCATGTGTCCACCCAGGACCGC 3318
 RESULT 13
 US-10-101-510-81
 ; Sequence 81, Application US/10101510
 ; Publication No. US20030148295A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WAN, JACKSON
 ; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 ; FILE REFERENCE: 15117.0012
 ; CURRENT APPLICATION NUMBER: US/101,510
 ; CURRENT FILING DATE: 2002-03-20
 ; PRIOR APPLICATION NUMBER: 60/276,947
 ; PRIOR FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 805
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 81
 ; LENGTH: 4473
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-101-510-81

Alignment Scores:
 Pred. No.: 0 Length: 4473
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservatives: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 15 Gaps: 1

US-09-493-480-7 (1-712) x US-10-101-510-81 (1-4473)

Qy 1 MetGluLeuAlaLeuCysArgThrGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
 Db 175 ATGGAGCTGGCGCTTGTGCGCTGGGGGCTCTCTCTCGCCCTCTTGGCCCCCGAGCC 234
 Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuLeuProAlaSerProGlu 40
 Db 235 GCGAGCACCAAGTGTGACCGGCGACAGATGAAGCTGCGGCTCTCTCGCAGTCCCGAG 294
 Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 Db 295 ACCACCTGGACATGCTCGCCACCTCTACCGGGCTGCGAGGTGTGTGCGAGGAACTTG 354
 Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 Db 355 GAACTCACCTACTGCGCCACCAATGCGAGCTGTCTCTCGCAGGATATCCAGGAGGTG 414
 Qy 81 GlnGlyTyrValLeuIleAlaHisGlnGlnValArgGlnValProLeuGlnArgLeuArg 100
 Db 415 CAGGGCTACGTGCTATCGCTCACACCAAGTGGAGCGAGGTCTCCACTGCGAGGCTGCGG 474
 Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAngly 120
 Db 475 ATTGTGGAGGACCCCGAGCTCTTTGAGGACAACTATGCCCCTGGCGTGTAGCAATGGA 534

Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
 Db 535 GACCCGCTGAACAATAACACCCCTGTGTACAGGGGCTCTCCAGAGGAGCTTCGGGAGCTG 594
 Qy 141 GlnLeuArgSerLeuThrGluIleLeuLeuGlyValLeuIleGlnArgAsnProGln 160
 Db 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCAGCGGAACCCAG 654
 Qy 161 LeuCysTyrGlnAspThrIleLeuThrPylsAspIlePheHisLeuAsnAsnGlnLeuAla 180
 Db 655 CTCTGCTACCAAGCACCGANTTTGTGGAAGGACATCTTCCACAAGAACACCAAGCTGGCT 714
 Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 Db 715 CTCACACTGATAGACCAACCGCTCTCGGGCTCTCCACCCCTGTCTCTCCGATGTGTAG 774
 Qy 201 GlySerArgCysTyrGlyLeuSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 Db 775 GCTCTCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTGAGGCTTGACGGCCTGTCTGT 834
 Qy 221 AlaGlyGlyCysAlaArgCysAlaGlyProLeuProThrAspCysCysHisGluGlnCys 240
 Db 835 GCGGCTGGCTGTGCGCCGCTGCAAGGGGCGACTGCCCACTGCTGCTGCCATGAGCAGTGT 894
 Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 Db 895 GCTGCCGCTGACCGGGCCCCAAGCCTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
 Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 Db 955 AGTGGCANTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
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 Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLeuCysSerLysProCysAlaArg 340
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 Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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 Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
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QY 705 GlyMetValHisArgHisArg 712
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RESULT 15

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; Sequence 45, Application US/10392113
; Publication No. US2003022493A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
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; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45
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Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	13	Gaps:	1

US-09-493-480-7 (1-712) x US-10-392-113-45 (1-4530)

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Db 271 ACCACCTGGACATGCTCCGCCACCTCTACCCGGGCTGCCAGGTGGTGACGGGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACCTCACCTTACCTGCCCAATGCCAGCTGTCTCTCTCTGCCAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
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QY 141 GlnLeuArgSerLeuThrGluIleLeuIleValLeuValLeuIleGlnArgAsnProGln 160
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QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GGCTCCCGCTGCTGGGGAGAGAGTCTGAGAGATGTCTGAGAGCTTCAGAGCCCTGACCGCCTGTCTGT 810
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Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyraAsnThrAspThrPheGlu	280
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Qy	281	SerMetProAsnProGluGlyArgGlyThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	991	TCCATGCCCAATCCCGAGGGCCGGTATACATTCCGCCCGCAGTGTGTGACTGCTGTGCC	1050
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	1051	TACAACTACTCTTCTACGGAGCTGGGATCTCGCACCCCTGGTCTGCCCTTCACACACAA	1110
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
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Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
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Db	1591	CCCTGGGACACAGCTCTTTGGGAACCCGACACAGCTCTGTCTCCACACTGCGCAACCGG	1650
Qy	501	GluAspGluCysValGlyGlnGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
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Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
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QY	601	ProSerGlyValIlyProAspLeuSerIyMetProIleTyrPlyPheProAspGluGlu	620
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=100 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HOLLERAN480 @CEN 1 1 141 @runat_07062004_152435_24765 -NCFU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	56.3	3768	2	US-08-625-101-1
2	89	56.3	3768	2	US-08-356-786-1
3	89	56.3	3768	4	US-09-811-115-2
4	89	56.3	4473	2	US-09-048-804-1
5	89	56.3	4473	3	US-09-056-105-26
6	89	56.3	4473	4	US-09-663-834A-3
7	89	56.3	4530	1	US-08-229-515A-9
8	89	56.3	4530	1	US-08-645-865-9
9	89	56.3	4530	4	US-09-167-322-4
10	89	56.3	4530	4	US-09-527-487-1
11	89	56.3	4530	4	US-09-877-177A-11
12	89	56.3	9274	4	US-09-811-115-1

13	84	53.2	3955	1	US-08-229-515A-14	Sequence 14, Appl
14	84	53.2	3955	1	US-08-645-865-14	Sequence 14, Appl
15	80	50.6	153	3	US-08-776-251-3	Sequence 3, Appl
16	80	50.6	201	4	US-09-200-355-3	Sequence 3, Appl
17	80	50.6	816	3	US-08-776-251-10	Sequence 10, Appl
18	80	50.6	2385	2	US-09-146-283-3	Sequence 3, Appl
19	80	50.6	2385	2	US-08-579-823A-3	Sequence 3, Appl
20	80	50.6	2385	3	US-09-344-195-3	Sequence 3, Appl
21	57	36.1	410	3	US-08-604-931-11	Sequence 11, Appl
22	57	36.1	410	3	US-09-363-639-11	Sequence 11, Appl
23	57	36.1	576	1	US-08-783-275-3	Sequence 3, Appl
24	57	36.1	576	1	US-08-727-708-3	Sequence 3, Appl
25	57	36.1	576	2	US-08-766-677-1	Sequence 1, Appl
26	57	36.1	576	2	US-08-843-951-1	Sequence 1, Appl
27	56	35.4	1830121	4	US-09-557-884-1	Sequence 1, Appl
28	56	35.4	1830121	4	US-09-643-990A-1	Sequence 3, Appl
29	54	34.2	5532	2	US-08-475-035-3	Sequence 3, Appl
30	54	34.2	5532	4	US-09-676-610B-17	Sequence 17, Appl
31	54	34.2	197496	4	US-09-877-177A-10	Sequence 10, Appl
32	53	33.5	2754	2	US-09-028-361A-1	Sequence 1, Appl
33	52	32.9	13321	4	US-08-956-171E-4	Sequence 4, Appl
34	51	32.3	5509	4	US-09-865-621A-1	Sequence 1, Appl
35	50	31.6	4411529	3	US-09-103-840A-2	Sequence 2, Appl
36	50	31.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl
37	49	31.0	2419	2	US-08-765-662-13	Sequence 13, Appl
38	49	31.0	2419	5	PCT-US95-08745-13	Sequence 13, Appl
39	49	31.0	2506	4	US-03-277-457-1	Sequence 1, Appl
40	49	31.0	2506	4	US-09-679-729-1	Sequence 1, Appl
41	49	31.0	3306	4	US-09-770-170-7	Sequence 7, Appl
42	49	31.0	10825	3	US-08-652-265-1	Sequence 1, Appl
43	49	31.0	10825	3	US-08-652-265-3	Sequence 3, Appl
44	49	31.0	10825	3	US-08-652-265-5	Sequence 5, Appl
45	49	31.0	10825	3	US-08-652-265-7	Sequence 7, Appl
46	49	31.0	10825	3	US-08-834-497A-1	Sequence 1, Appl
47	49	31.0	10825	3	US-08-834-497A-3	Sequence 3, Appl
48	49	31.0	10825	3	US-08-834-497A-5	Sequence 5, Appl
49	49	31.0	10825	3	US-08-834-497A-7	Sequence 7, Appl
50	49	31.0	10825	3	US-09-503-444A-1	Sequence 1, Appl
51	49	31.0	10825	3	US-09-503-444A-3	Sequence 3, Appl
52	49	31.0	10825	3	US-09-503-444A-5	Sequence 5, Appl
53	49	31.0	10825	3	US-09-503-444A-7	Sequence 7, Appl
54	49	31.0	12146	4	US-09-277-457-27	Sequence 27, Appl
55	49	31.0	12146	4	US-09-679-729-27	Sequence 27, Appl
56	49	31.0	35100	1	US-08-306-691B-19	Sequence 19, Appl
57	49	31.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl
58	49	31.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
59	49	31.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
60	49	31.0	246240	2	US-08-724-394A-22	Sequence 22, Appl
61	48.5	30.7	267	4	US-09-313-294A-1859	Sequence 1859, Ap
62	48.5	30.7	467	4	US-09-621-976-2248	Sequence 2248, Ap
63	48.5	30.7	3787	4	US-08-956-171E-375	Sequence 375, App
64	48	30.4	1284	4	US-09-894-844-106	Sequence 106, App
65	48	30.4	4422	4	US-09-166-350-1	Sequence 1, Appl
66	48	30.4	7970	1	US-08-135-511-31	Sequence 31, Appl
67	48	30.4	7970	1	US-08-187-453-31	Sequence 31, Appl
68	48	30.4	7970	1	US-08-562-985A-7	Sequence 7, Appl
69	48	30.4	24979	2	US-08-147-777-3	Sequence 3, Appl
70	48	30.4	24979	3	US-08-452-872-3	Sequence 3, Appl
71	48	30.4	24979	5	PCT-US93-03985-3	Sequence 3, Appl
72	48	30.4	35100	2	US-08-770-379-17	Sequence 17, Appl
73	48	30.4	35100	3	US-08-757-669A-17	Sequence 17, Appl
74	48	30.4	35100	4	US-09-230-371A-17	Sequence 17, Appl
75	47.5	30.1	564	4	US-09-134-001C-2343	Sequence 2343, Ap
76	47.5	30.1	1913	4	US-09-016-434-1314	Sequence 1314, Ap
77	47.5	30.1	2467	4	US-09-872-733A-3	Sequence 3, Appl
78	47.5	30.1	4338	4	US-09-872-733A-1	Sequence 1, Appl
79	47.5	30.1	8366	4	US-09-872-733A-6	Sequence 6, Appl
80	47.5	30.1	11561	1	US-08-450-332-1	Sequence 1, Appl
81	47.5	30.1	11561	2	US-08-637-640-1	Sequence 1, Appl
82	47.5	30.1	11561	3	US-09-004-406C-1	Sequence 1, Appl
83	47.5	30.1	33000	3	US-09-215-694-18	Sequence 18, Appl
84	47	29.7	305	3	US-09-289-843A-21	Sequence 21, Appl
85	47	29.7	305	4	US-09-088-337B-21	Sequence 21, Appl

c 86 47 29.7 558 4 US-09-280-116-185 Sequence 185, App
87 47 29.7 564 4 US-09-489-039A-6153 Sequence 6153, App
88 47 29.7 564 4 US-09-621-976-15297 Sequence 15297, A
89 47 29.7 1563 4 US-09-252-991A-12880 Sequence 12880, A
90 47 29.7 1623 4 US-09-252-991A-12572 Sequence 12572, A
91 47 29.7 1638 4 US-09-252-991A-16400 Sequence 16400, A
92 47 29.7 1917 4 US-09-499-203-15 Sequence 15, Appl
93 47 29.7 2229 4 US-09-252-991A-16088 Sequence 16088, A
94 47 29.7 2532 4 US-09-252-991A-12912 Sequence 12912, A
95 47 29.7 3489 4 US-09-252-991A-16193 Sequence 16193, A
96 47 29.7 3970 4 US-09-499-203-14 Sequence 14, Appl
97 47 29.7 4066 4 US-09-499-203-16 Sequence 16, Appl
98 47 29.7 6204 4 US-09-499-203-20 Sequence 20, Appl
99 47 29.7 7387 4 US-09-499-203-17 Sequence 17, Appl
100 47 29.7 9321 4 US-09-499-203-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3765
US-08-625-101-1

Alignment Scores: 6.95e-05 Length: 3768
Pred. No.: 89.00 Matches: 20
Score: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 2 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-625-101-1 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACCATGACATGGGGGAC 3048
Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057
RESULT 2
US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3768
; OTHER INFORMATION: /note= "product = "cerB-b2"
US-08-356-786-1

Alignment Scores: 6.95e-05 Length: 3768
Pred. No.: 89.00 Matches: 20
Score: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 2 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-356-786-1 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACCATGACATGGGGGAC 3048

Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGCAGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30

Db 3049 CTGGTGGAT 3057

RESULT 3

US-09-811-115-2

; Sequence 2, Application US/09811115

; Patent No. 6632979

; GENERAL INFORMATION:

; APPLICANT: Erickson, Sharon

; APPLICANT: Schwall, Ralph

; APPLICANT: King, Kathleen

; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL

; FILE REFERENCE: GENENT.034A

; CURRENT APPLICATION NUMBER: US/09/811,115

; CURRENT FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/189,844

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 3768

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-811-115-2

Alignment Scores:

Pred. No.: 6.95e-05 Length: 3768

Score: 89.00 Matches: 20

Percent Similarity: 86.96% Conservative: 0

Best Local Similarity: 86.96% Mismatches: 1

Query Match: 56.33% Indels: 2

DB: 4 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-811-115-2 (1-3768)

Qy 10 AlaserProLeu-----ThrsTyrArgSerLeuLeuGluAspAspMetGlyAsp 27

Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGCAGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30

Db 3049 CTGGTGGAT 3057

RESULT 4

US-09-048-804-1

; Sequence 1, Application US/09048804

; Patent No. 5968748

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF

; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748:ris LLP

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb diskette

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/048,804

; FILING DATE: Herewith

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul K. Legaard

; REGISTRATION NUMBER: 38,534

; REFERENCE/DOCKET NUMBER: ISIS-2913

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4473 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Unknown

; ANTI-SENSE: NO

US-09-048-804-1

Alignment Scores:

Pred. No.: 8.75e-05 Length: 4473

Score: 89.00 Matches: 20

Percent Similarity: 86.96% Conservative: 0

Best Local Similarity: 86.96% Mismatches: 1

Query Match: 56.33% Indels: 2

DB: 2 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-048-804-1 (1-4473)

Qy 10 AlaserProLeu-----ThrsTyrArgSerLeuLeuGluAspAspMetGlyAsp 27

Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGCAGATGACATGGGGGAC 3222

Qy 28 LeuValAsp 30

Db 3223 CTGGTGGAT 3231

RESULT 5

US-09-056-105-26

; Sequence 26, Application US/09056105

; Patent No. 6287569

; GENERAL INFORMATION:

; APPLICANT: KIPPS, THOMAS J.

; APPLICANT: WU, YUNQI

; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

; TITLE OF INVENTION: PROCESSING

; FILE REFERENCE: 233/221

; CURRENT APPLICATION NUMBER: US/09/056,105

; CURRENT FILING DATE: 1998-04-06

; EARLIER APPLICATION NUMBER: 60/043,467

; EARLIER FILING DATE: 1997-04-10

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 4473

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-056-105-26

Alignment Scores:

Pred. No.: 8.75e-05 Length: 4473

Score: 89.00 Matches: 20

Percent Similarity: 86.96% Conservative: 0

Best Local Similarity: 86.96% Mismatches: 1

Query Match: 56.33% Indels: 2

DB: 3 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-056-105-26 (1-4473)

Qy 10 AlaserProLeu-----ThrsTyrArgSerLeuLeuGluAspAspMetGlyAsp 27

Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGCAGATGACATGGGGGAC 3222

Qy 28 LeuValAsp 30

Db 3223 CTGGTGGAT 3231

RESULT 6

US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)...(3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 8,75e-05 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 4 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-663-834A-3 (1-4473)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCACGTCCCTTGGACAGCACCTTCTACCGCTGAGGAGCAGTGCATGGGGGAC 3222

Qy 28 LeuValasp 30
Db 3223 CTGGTGGAT 3231

RESULT 7

US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-9

Alignment Scores:
Pred. No.: 8,75e-05 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 4 Gaps: 1

; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-9

Alignment Scores:
Pred. No.: 8,9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 1 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-229-515A-9 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3139 GCACGTCCCTTGGACAGCACCTTCTACCGCTGAGGAGCAGTGCATGGGGGAC 3198

Qy 28 LeuValasp 30
Db 3199 CTGGTGGAT 3207

RESULT 8

US-08-645-865-9
; Sequence 9, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-9

Alignment Scores:
Pred. No.: 8,9e-05 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 1 Gaps: 1

Qy 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||
Db 10 GACACAGGGGTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCC 54

; MOLECULE TYPE: CDNA


```

; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSP-HER-2 fusion gene; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-344-195-3

Alignment Scores:
Pred. No.: 0.00124 Length: 2385
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.63% Indels: 0
DB: 3 Gaps: 0

SEQ3-SEQ4 (1-30) x US-09-344-195-3 (1-2385)

Oy 1 AsplygGlyCysProAlaGluInArgAlaSerProLeuThrSer 15
Db 1925 GACAAGGGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTCC 1969

RESULT 21
US-08-604-991-11
; Sequence 11, Application US/08604991
; Patent No. 6001565
; GENERAL INFORMATION:
; APPLICANT: Fox, Andrew J.
; APPLICANT: Jones, Dennis Mackay
; TITLE OF INVENTION: Detection and Speciation of
; TITLE OF INVENTION: Campylobacter
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,991
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB94/01967
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318751.6
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0040000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-317-2600
; TELEFAX: 202-317-2540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-604-991-11

Alignment Scores:
Pred. No.: 0.893 Length: 410
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: 3 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-604-991-11 (1-410)

Oy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 225 AGCCCTACAGATTCCAAGTTTATCGCACCTGATGGAGGAGGAGGACATGGAGACATT 284

Oy 29 Valasp 30
Db 285 GTGGAT 290

RESULT 22
US-09-363-639-11
; Sequence 11, Application US/09363639
; Patent No. 6080547
; GENERAL INFORMATION:
; APPLICANT: Fox, Andrew J.
; APPLICANT: Jones, Dennis Mackay
; TITLE OF INVENTION: Detection and Speciation of
; TITLE OF INVENTION: Campylobacter
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/363,639
FILING DATE: 30-JUL-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/604,991
FILING DATE: 29-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB94/01967
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9318751.6
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Remond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0040001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-317-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-363-639-11

Alignment Scores:
Pred. No.: 0.893 Length: 410
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: 3 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-363-639-11 (1-410)

QY 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
|||||
DB 225 AGCCCTACAGATTCACAGTTTATCCACCTGATGAGGAGGACATGGACACATT 284
QY 29 Valasp 30
|||||
DB 285 GTGGAT 290

RESULT 23
US-08-783-275-3
Sequence 3, Application US/08783275
Patent No. 5766859
GENERAL INFORMATION:
APPLICANT: Vojdani, Aristio
APPLICANT: Mordechai, Eli
TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS
TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,275
FILING DATE: 15-JAN-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/727,708
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: IMSCI.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-783-275-3

Alignment Scores:
Pred. No.: 1.41 Length: 576
Score: 57.00 Matches: 12
Percent Similarity: 77.27% Conservative: 5
Best Local Similarity: 54.55% Mismatches: 3
Query Match: 36.08% Indels: 2
DB: 1 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-783-275-3 (1-576)

QY 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
|||||
DB 222 AGCCCTACAGATTCACAGTTTATCCACCTGATGAGGAGGACATGGACACATT 281
QY 29 Valasp 30
|||||
DB 282 GTGGAT 287

RESULT 24
US-08-727-708-3
Sequence 3, Application US/08727708
Patent No. 5776690
GENERAL INFORMATION:
APPLICANT: Vojdani, Aristio
APPLICANT: Mordechai, Eli
TITLE OF INVENTION: RIBONUCLEASE L INHIBITOR AS
TITLE OF INVENTION: AN INDICATOR OF CHRONIC FATIGUE SYNDROM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,708
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: IMSCI.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550

```
TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
  LENGTH: 576 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
US-08-727-708-3

Alignment Scores:
Pred. No.: 1.41      Length: 576
Score: 57.00        Matches: 12
Percent Similarity: 77.27%  Conservative: 5
Best Local Similarity: 54.55%  Mismatches: 3
Query Match: 36.08%      Indels: 2
DB: 1                Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-727-708-3 (1-576)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 222 AGCCCTACAGATTCCAGTTTATCGCACCTGATGGAGGAGGAGGACATGGAGACATT 281
Qy 29 Valasp 30
Db 282 GTGGAT 287

RESULT 25
US-08-766-677-1
; Sequence 1, Application US/08766677
; Patent No. 5830668
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: Detection of Chronic Fatigue
; TITLE OF INVENTION: Syndrome
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIORITY APPLICATION NUMBER: US/08/766,677
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: IMSCI.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-766-677-1

Alignment Scores:
Pred. No.: 1.41      Length: 576
Score: 57.00        Matches: 12
Percent Similarity: 77.27%  Conservative: 5
Best Local Similarity: 54.55%  Mismatches: 3
Query Match: 36.08%      Indels: 2
DB: 1                Gaps: 1
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TELEFAX: 619-235-0176
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
  LENGTH: 576 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
US-08-727-708-3

Alignment Scores:
Pred. No.: 1.41      Length: 576
Score: 57.00        Matches: 12
Percent Similarity: 77.27%  Conservative: 5
Best Local Similarity: 54.55%  Mismatches: 3
Query Match: 36.08%      Indels: 2
DB: 1                Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-766-677-1 (1-576)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 222 AGCCCTACAGATTCCAGTTTATCGCACCTGATGGAGGAGGAGGACATGGAGACATT 281
Qy 29 Valasp 30
Db 282 GTGGAT 287

RESULT 26
US-08-843-951-1
; Sequence 1, Application US/08843951
; Patent No. 5853996
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: Detection of Chronic Fatigue
; TITLE OF INVENTION: Syndrome
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive Sixteenth Flo
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIORITY APPLICATION NUMBER: US/08/843,951
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: IMSCI.002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714/760-0404
; TELEFAX: 714/760-9503
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-843-951-1

Alignment Scores:
Pred. No.: 1.41      Length: 576
Score: 57.00        Matches: 12
Percent Similarity: 77.27%  Conservative: 5
Best Local Similarity: 54.55%  Mismatches: 3
Query Match: 36.08%      Indels: 2
DB: 1                Gaps: 1
```


GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/475.035
; APPLICATION NUMBER: US/08/475.035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3816
; US-08-475-035-3

Alignment Scores:
Pred. No.: 94.7 Length: 5532
Score: 54.00 Matches: 11
Percent Similarity: 77.27% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 34.18% Indels: 2
DB: 2 Gaps: 1

SEQ3-SEQ4 (1-30) x US-08-475-035-3 (1-5532)

Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 3157 AGTCCTACAGACTCCAACTTCTACCGTCCCTGATGATGAGAGACATGGACGCGTG 3216
Qy 29 ValAsp 30
Db 3217 GTGGAT 3222

RESULT 30

US-09-676-610B-17
; Sequence 17, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676.610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182

; SEQ ID NO 17
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (187)...(3819)
US-09-676-610B-17
Alignment Scores:
Pred. No.: 94.7 Length: 5532
Score: 54.00 Matches: 11
Percent Similarity: 77.27% Conservative: 6
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 34.18% Indels: 2
DB: 4 Gaps: 1
SEQ3-SEQ4 (1-30) x US-09-676-610B-17 (1-5532)
Qy 11 SerProLeuThrSer-----TyrArgSerLeuLeuGluAspAspMetGlyAspLeu 28
Db 3157 AGTCCTACAGACTCCAACTTCTACCGTCCCTGATGATGAGAGACATGGACGCGTG 3216
Qy 29 ValAsp 30
Db 3217 GTGGAT 3222
Search completed: June 8, 2004, 08:59:40
Job time : 742 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 06:43:09 ; Search time 267 Seconds
(without alignments)
512.584 Million cell updates/sec

Title: SEQ3-SEQ4

Perfect score: 158

Sequence: 1 DKGCPAQRASPLTYSRLLEDDMDGLVD 30

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Delop 6.0	Delext 7.0	

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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18:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
19:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	89	56.3	1115	13	US-09-925-298-165	Sequence 165, App
2	89	56.3	1115	15	US-10-102-806-165	Sequence 165, App
3	89	56.3	1713	15	US-10-378-393-14	Sequence 14, Appl
4	89	56.3	1755	9	US-09-930-125-6	Sequence 6, Appl
5	89	56.3	1767	9	US-09-930-125-4	Sequence 4, Appl
6	89	56.3	1773	9	US-09-930-125-7	Sequence 7, Appl
7	89	56.3	1806	9	US-09-930-125-5	Sequence 5, Appl
8	89	56.3	2411	15	US-10-378-393-10	Sequence 10, Appl
9	89	56.3	3765	15	US-10-207-498-5	Sequence 5, Appl
10	89	56.3	3768	9	US-09-811-123-8	Sequence 8, Appl
11	89	56.3	3768	9	US-09-811-115-2	Sequence 2, Appl
12	89	56.3	3768	9	US-09-854-356-9	Sequence 9, Appl
13	89	56.3	3768	9	US-09-930-125-1	Sequence 1, Appl
14	89	56.3	3768	13	US-09-984-092-3	Sequence 3, Appl
15	89	56.3	3768	13	US-10-280-576-3	Sequence 3, Appl
16	89	56.3	3768	13	US-09-765-973-1	Sequence 1, Appl
17	89	56.3	3768	15	US-10-313-644-1	Sequence 1, Appl
18	89	56.3	4473	10	US-09-441-411-5	Sequence 5, Appl
19	89	56.3	4473	15	US-10-146-473-32	Sequence 32, Appl
20	89	56.3	4473	15	US-10-207-655-44	Sequence 44, Appl
21	89	56.3	4473	15	US-10-101-510-81	Sequence 81, Appl
22	89	56.3	4530	9	US-09-877-177-11	Sequence 11, Appl
23	89	56.3	4530	13	US-10-392-113-45	Sequence 45, Appl
24	89	56.3	4530	13	US-10-426-836-11	Sequence 11, Appl
25	89	56.3	4530	15	US-10-177-293-125	Sequence 125, App
26	89	56.3	4530	15	US-10-007-926A-119	Sequence 119, App
27	89	56.3	4530	15	US-10-338-730-1	Sequence 1, Appl
28	89	56.3	4530	15	US-10-101-510-124	Sequence 124, App
29	89	56.3	4530	16	US-10-116-275-131	Sequence 131, App
30	89	56.3	4530	16	US-10-272-437A-27	Sequence 27, Appl
31	89	56.3	4530	16	US-10-117-937-595	Sequence 595, App
32	89	56.3	4530	16	US-10-159-563-208	Sequence 208, App
33	89	56.3	4530	16	US-10-435-696-10	Sequence 10, Appl
34	89	56.3	4543	10	US-09-769-508-1	Sequence 1, Appl
35	89	56.3	4543	10	US-09-971-392-70	Sequence 70, Appl
36	89	56.3	4642	15	US-10-198-846-10896	Sequence 10896, A
37	89	56.3	9274	9	US-09-811-123-7	Sequence 7, Appl
38	89	56.3	9274	9	US-09-811-115-1	Sequence 1, Appl
39	84	53.2	3955	9	US-09-870-759-117	Sequence 117, App
40	84	53.2	3955	9	US-09-854-356-10	Sequence 10, Appl
41	84	53.2	3955	10	US-09-751-708A-117	Sequence 117, App
42	80	50.6	201	14	US-10-109-213-3	Sequence 3, Appl
43	80	50.6	884	16	US-10-412-804A-7	Sequence 7, Appl
44	80	50.6	1479	16	US-10-412-804A-1	Sequence 1, Appl
45	80	50.6	2164	16	US-10-412-804A-5	Sequence 5, Appl
46	80	50.6	3771	9	US-09-854-356-11	Sequence 11, Appl
47	74	46.8	2149	16	US-10-412-804A-9	Sequence 9, Appl
48	63	39.9	249	9	US-09-960-352-4186	Sequence 4186, Ap
49	57	36.1	1829	13	US-10-425-114-31106	Sequence 31106, A
50	56	35.4	1830121	15	US-10-329-960-1	Sequence 1, Appl
51	56	35.4	1830121	16	US-10-329-670-1	Sequence 1, Appl
52	55.5	35.1	441	9	US-09-864-761-3956	Sequence 3956, Ap
53	55.5	35.1	6236	13	US-10-381-327-16	Sequence 16, Appl
54	55	34.8	492	10	US-09-918-995-29035	Sequence 29035, A
55	54	34.2	376	13	US-10-027-632-55589	Sequence 55589, A
56	54	34.2	376	13	US-10-027-632-55589	Sequence 311744, A
57	54	34.2	376	16	US-10-027-632-55589	Sequence 55589, A
58	54	34.2	376	16	US-10-027-632-311744	Sequence 311744, A
59	54	34.2	520	9	US-09-867-701-7156	Sequence 7156, Ap
60	54	34.2	600	9	US-09-864-761-15913	Sequence 15913, A
61	54	34.2	3633	9	US-09-725-433-1	Sequence 1, Appl
62	54	34.2	3633	13	US-10-236-417-75	Sequence 75, Appl
63	54	34.2	5264	9	US-09-920-300A-1731	Sequence 1731, Ap
64	54	34.2	5264	14	US-10-033-528-1731	Sequence 1731, Ap
65	54	34.2	5264	15	US-10-099-926-1731	Sequence 73, Ap
66	54	34.2	5367	13	US-10-236-417-73	Sequence 73, Appl
67	54	34.2	5532	13	US-10-387-252-1	Sequence 1, Appl
68	54	34.2	5532	13	US-10-388-360-300	Sequence 300, App
69	54	34.2	5532	15	US-10-007-926A-137	Sequence 137, App
70	54	34.2	5532	15	US-10-101-510-95	Sequence 95, Appl
71	54	34.2	5532	16	US-10-380-931-17	Sequence 17, Appl
72	54	34.2	10058	9	US-09-974-298-98	Sequence 98, Appl


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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-14
```

```
Alignment Scores:
Pred. No.: 4.59e-05 Length: 1713
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1
```

SEQ3-SEQ4 (1-30) x US-10-378-393-14 (1-1713)

```
Oy 10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 934 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 993
Oy 28 LeuValAsp 30
Db 994 CTGGTGGAT 1002
```

RESULT 4

US-09-930-125-6

; Sequence 6, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930.125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 1755

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-930-125-6

```
Alignment Scores:
Pred. No.: 4.73e-05 Length: 1755
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1
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SEQ3-SEQ4 (1-30) x US-09-930-125-6 (1-1755)

```
Oy 10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 967 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1026
Oy 28 LeuValAsp 30
Db 1027 CTGGTGGAT 1035
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RESULT 5

US-09-930-125-4

; Sequence 4, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

```
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930.125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-125-4
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```
Alignment Scores:
Pred. No.: 4.77e-05 Length: 1767
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1
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SEQ3-SEQ4 (1-30) x US-09-930-125-4 (1-1767)

```
Oy 10 AlaSerProLeu-----ThrSerTyArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 967 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1026
Oy 28 LeuValAsp 30
Db 1027 CTGGTGGAT 1035
```

RESULT 6

US-09-930-125-7

; Sequence 7, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930.125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 1773

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-930-125-7

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Alignment Scores:
Pred. No.: 4.78e-05 Length: 1773
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1
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SEQ3-SEQ4 (1-30) x US-09-930-125-7 (1-1773)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 991 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1050

QY 28 LeuValasp 30
Db 1051 CTGGTGGAT 1059

RESULT 7

US-09-930-125-5
; Sequence 5, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedwick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-125-5

Alignment Scores:
Pred. No.: 4.89e-05 Length: 1806
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-5 (1-1806)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 1024 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1083

QY 28 LeuValasp 30
Db 1084 CTGGTGGAT 1092

RESULT 8

US-10-378-393-10
; Sequence 10, Application US/10178393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-378-393-10

Alignment Scores:
Pred. No.: 6.9e-05 Length: 2411
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-378-393-10 (1-2411)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 1632 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 1691

QY 28 LeuValasp 30
Db 1692 CTGGTGGAT 1700

RESULT 9

US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; AND MODULATING INTERACTIONS BETWEEN HERGULIN AND HER3
; FILE REFERENCE: 30448.103-US-UI
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5

Alignment Scores:
Pred. No.: 0.000117 Length: 3765
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-207-498-5 (1-3765)

QY 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048

QY 28 LeuValasp 30
Db 3049 CTGGTGGAT 3057

RESULT 10

US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall

```

; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ETBB
; FILE REFERENCE: ANTIBODY-MAYTANSINOID CONJUGATES
; CURRENT APPLICATION NUMBER: 073A2
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-811-123-8 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 11
US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-811-115-2 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3048

Qy 28 LeuValAsp 30
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```

Db 3049 CTGGTGGAT 3057

RESULT 12
US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheeysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; OTHER INFORMATION: human HER-2/neu protein
; NAME/KEY: misc_feature
; LOCATION: (1)..(1959)
; OTHER INFORMATION: extracellular domain (BCD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2026)..(3765)
; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3765)
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (delta PD) of human HER-2/neu
US-09-854-356-9

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-854-356-9 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 13
US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
```

```

; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-930-125-1

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-930-125-1 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 14
US-09-984-092-3
; Sequence 3, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P101PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
US-09-984-092-3

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-984-092-3 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 15
US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-576-3

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-280-576-3 (1-3768)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048

Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 16
US-09-765-973-1
; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; TITLE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1

Alignment Scores:
Pred. No.: 0.000117 Length: 3768
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-765-973-1 (1-3768)
```

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048
Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 17
US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1

Alignment Scores: Length: 3768
Pred. No.: 0.000117
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservativeness: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-313-644-1 (1-3768)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 2989 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3048
Qy 28 LeuValAsp 30
Db 3049 CTGGTGGAT 3057

RESULT 18
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US2003008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores: Length: 4473
Pred. No.: 0.000144

Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservativeness: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-441-411-5 (1-4473)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 19
US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores: Length: 4473
Pred. No.: 0.000144
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservativeness: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-146-473-32 (1-4473)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 20
US-10-207-655-44
; Sequence 44, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44


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; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44

Alignment Scores:
Pred. No.: 0.000144 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-207-655-44 (1-4473)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 21
US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81

Alignment Scores:
Pred. No.: 0.000144 Length: 4473
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-101-510-81 (1-4473)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 3163 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3222
Qy 28 LeuValAsp 30
Db 3223 CTGGTGGAT 3231

RESULT 22
US-09-877-177-11
; Sequence 11, Application US/09877177
; Publication No. US20020192652A1
; GENERAL INFORMATION:
; APPLICANT: Peter V. Danenberg et al.
; TITLE OF INVENTION: Method of determining Epidermal Growth
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177
; CURRENT FILING DATE: 2001-06-11
```

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177-11

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 9 Gaps: 1

SEQ3-SEQ4 (1-30) x US-09-877-177-11 (1-4530)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 23
US-10-392-113-45
; Sequence 45, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-392-113-45

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-392-113-45 (1-4530)
Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuGluAspAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207
```

```
RESULT 24
US-10-426-836-11
; Sequence 11, Application US/10426836
; Publication No. US20030211530A1
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/169
; CURRENT APPLICATION NUMBER: US/10/426,836
; PRIORITY FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-836-11

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 13 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-426-836-11 (1-4530)
Qy 10 AlaserProleu-----ThrSerTyArgSerLeuLeuGluAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 25
US-10-177-293-125
; Sequence 125, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIORITY FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIORITY FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIORITY FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIORITY FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
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; PRIORITY FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIORITY FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIORITY FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-125

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-177-293-125 (1-4530)
Qy 10 AlaserProleu-----ThrSerTyArgSerLeuLeuGluAspMetGlyAsp 27
Db 3139 GCCAGTCCCTTGGACAGCACCCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198
Qy 28 LeuValAsp 30
Db 3199 CTGGTGGAT 3207

RESULT 26
US-10-007-926A-119
; Sequence 119, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007.926A
; PRIORITY FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIORITY FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral
; OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived
; OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
US-10-007-926A-119

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-007-926A-119 (1-4530)
Qy 10 AlaserProleu-----ThrSerTyArgSerLeuLeuGluAspMetGlyAsp 27
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Db 3139 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198

Qy 28 LeuValasp 30
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Db 3199 CTGGTGGAT 3207

RESULT 27

US-10-338-730-1
; Sequence 1, Application US/10338730
; Publication No. US20030147905A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS
; FILE REFERENCE: 5017C
; CURRENT APPLICATION NUMBER: US/10/338,730
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US 09/527,487
; PRIOR FILING DATE: 2002-03-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
; OTHER INFORMATION:
US-10-338-730-1

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-338-730-1 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
|||||

Db 3139 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198

Qy 28 LeuValasp 30
|||||

Db 3199 CTGGTGGAT 3207

RESULT 28

US-10-101-510-124
; Sequence 124, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-124

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20

Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 15 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-101-510-124 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
|||||

Db 3139 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198

Qy 28 LeuValasp 30
|||||

Db 3199 CTGGTGGAT 3207

RESULT 29

US-10-116-275-131
; Sequence 131, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087 Compositions Targeting Peyer's Patches and M Cell Receptors
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-131

Alignment Scores:
Pred. No.: 0.000146 Length: 4530
Score: 89.00 Matches: 20
Percent Similarity: 86.96% Conservative: 0
Best Local Similarity: 86.96% Mismatches: 1
Query Match: 56.33% Indels: 2
DB: 16 Gaps: 1

SEQ3-SEQ4 (1-30) x US-10-116-275-131 (1-4530)

Qy 10 AlaSerProLeu-----ThrSerTyrArgSerLeuLeuGluAspAspMetGlyAsp 27
|||||

Db 3139 GCCAGTCCCTGGACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGAC 3198

Qy 28 LeuValasp 30
|||||

Db 3199 CTGGTGGAT 3207

RESULT 30

US-10-272-437A-27
; Sequence 27, Application US/10272437A
; Publication No. US20030216309A1
; GENERAL INFORMATION:
; APPLICANT: Krag, David N.
; APPLICANT: Pero, Stephanie C.
; APPLICANT: Oligino, Lyn
; TITLE OF INVENTION: BINDING PEPTIDES SPECIFIC FOR THE EXTRACELLULAR DOMAIN OF ERBB2
; FILE REFERENCE: V00139.70056.US
; CURRENT APPLICATION NUMBER: US/10/272,437A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,183
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 46

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-437A-27

Alignment Scores:
Pred. No.:          Length:      4530
Score:              Matches:     20
                    Conservative: 0
Best Local Similarity: 86.96%
Query Match:        Mismatches:   1
DB:                  Indels:       2
                    Gaps:         1

SEQ3-SEQ4 (1-30) x US-10-272-437A-27 (1-4530)

Qy    10 AlasexProLeu-----ThrSerTyrArgSerLeuLeuGluAspMetGlyAsp 27
      |||||
Db    3139 GCCAGTCCTTGACACAGCACCTTCTACCGCTCACTGCTGGAGGCCGATGCATGGGGGAC 3198

Qy    28 LeuValasp 30
      |||||
Db    3199 CTGGTGGAT 3207
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Search completed: June 8, 2004, 09:24:13
Job time : 284 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 04:50:51 ; Search time 62 Seconds
(without alignments)
268.525 Million cell updates/sec

Title: SEQ3-SEQ5

Perfect score: 159

Sequence: 1 DKGCPAQRASPLTSQNEGLGPASPLDSTP 30

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	52.8	2385	2	US-09-146-283-3
2	84	52.8	2385	3	US-08-579-823A-3
3	84	52.8	2385	3	US-09-344-195-3
4	80	50.3	153	3	US-08-776-251-3
5	80	50.3	201	4	US-09-200-355-3
6	80	50.3	816	3	US-08-776-251-10
7	80	50.3	3768	2	US-08-625-101-1
8	80	50.3	3768	2	US-08-356-786-1
9	80	50.3	3768	4	US-09-811-115-2
10	80	50.3	4473	2	US-09-048-804-1
11	80	50.3	4473	3	US-09-056-105-26
12	80	50.3	4473	4	US-09-663-834A-3

13	80	50.3	4530	1	US-08-229-515A-9	Sequence 9, Appli
14	80	50.3	4530	1	US-08-645-865-9	Sequence 9, Appli
15	80	50.3	4530	1	US-09-167-322-4	Sequence 4, Appli
16	80	50.3	4530	4	US-09-527-487-1	Sequence 1, Appli
17	80	50.3	4530	4	US-09-877-177A-11	Sequence 11, Appli
18	80	50.3	9274	4	US-09-811-115-1	Sequence 1, Appli
19	74	46.5	3955	1	US-08-229-515A-14	Sequence 14, Appli
20	74	46.5	3955	1	US-08-645-865-14	Sequence 14, Appli
C 21	59	37.1	11282	4	US-09-754-250-3	Sequence 3, Appli
C 22	58.5	36.8	634	1	US-08-451-947-1	Sequence 1, Appli
C 23	58.5	36.8	634	2	US-08-424-826A-1	Sequence 1, Appli
C 24	58.5	36.8	634	3	US-08-928-894-1	Sequence 1, Appli
C 25	58.5	36.8	634	4	US-08-450-842-1	Sequence 1, Appli
C 26	58.5	36.8	634	4	US-08-451-390-1	Sequence 1, Appli
C 27	58.5	36.8	634	5	PCT-US91-06950-1	Sequence 1, Appli
C 28	58.5	36.8	1404	1	US-07-796-106-22	Sequence 22, Appli
C 29	58.5	36.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 30	58.5	36.8	441529	3	US-09-103-840A-1	Sequence 1, Appli
C 31	57	35.8	1938	4	US-09-547-435-25	Sequence 25, Appli
C 32	57	35.8	2316	4	US-09-547-435-27	Sequence 27, Appli
C 33	57	35.8	2604	4	US-09-547-435-23	Sequence 23, Appli
C 34	57	35.8	3384	4	US-09-547-435-29	Sequence 29, Appli
C 35	55.5	34.9	2691	4	US-09-020-743-1	Sequence 1, Appli
C 36	55	34.6	960	3	US-08-651-136C-1	Sequence 1, Appli
C 37	55	34.6	960	4	US-09-229-911A-1	Sequence 1, Appli
C 38	55	34.6	4092	3	US-09-306-595C-5	Sequence 5, Appli
C 39	55	34.6	4092	4	US-09-925-388-5	Sequence 5, Appli
C 40	55	34.6	5046	4	US-09-548-938A-5	Sequence 5, Appli
C 41	54.5	34.3	824	4	US-09-312-283C-369	Sequence 369, App
C 42	54	34.0	883	4	US-09-833-381-210	Sequence 210, App
C 43	53.5	33.6	685	1	US-08-451-947-7	Sequence 7, Appli
C 44	53.5	33.6	685	2	US-08-424-826A-7	Sequence 7, Appli
C 45	53.5	33.6	685	3	US-08-928-694-7	Sequence 7, Appli
C 46	53.5	33.6	685	4	US-08-450-842-7	Sequence 7, Appli
C 47	53.5	33.6	685	4	US-08-451-390-7	Sequence 7, Appli
C 48	53.5	33.6	685	5	PCT-US91-06950-7	Sequence 9, Appli
C 49	53.5	33.6	1190	1	US-08-451-947-9	Sequence 9, Appli
C 50	53.5	33.6	1190	2	US-08-424-826A-9	Sequence 9, Appli
C 51	53.5	33.6	1190	3	US-08-928-694-9	Sequence 9, Appli
C 52	53.5	33.6	1190	4	US-08-450-842-9	Sequence 9, Appli
C 53	53.5	33.6	1190	4	US-08-451-390-9	Sequence 9, Appli
C 54	53.5	33.6	1190	5	PCT-US91-06950-9	Sequence 9, Appli
C 55	53.5	33.6	32998	4	US-09-408-020-1	Sequence 1, Appli
C 56	53	33.3	963	4	US-09-252-991A-6814	Sequence 6814, Ap
C 57	53	33.3	1081	2	US-08-708-856A-13	Sequence 13, Appli
C 58	53	33.3	1081	3	US-09-287-375-13	Sequence 13, Appli
C 59	53	33.3	1081	4	US-09-455-406-13	Sequence 13, Appli
C 60	53	33.3	1368	4	US-09-328-352-430	Sequence 430, App
C 61	53	33.3	7174	4	US-08-961-527-189	Sequence 189, App
C 62	53	33.3	12047	2	US-09-022-461-1	Sequence 1, Appli
C 63	53	33.3	12047	3	US-09-033-556-3	Sequence 3, Appli
C 64	53	33.3	12047	4	US-09-474-699-11	Sequence 11, Appli
C 65	53	33.3	12047	4	US-09-151-376-3	Sequence 3, Appli
C 66	52.5	33.0	5766	4	US-09-566-921-39	Sequence 39, Appli
C 67	52	32.7	32000	4	US-10-027-983-11	Sequence 11, Appli
C 68	51.5	32.4	34063	4	US-09-453-702B-96	Sequence 96, Appli
C 69	51	32.1	873	4	US-09-489-039A-1911	Sequence 1911, Ap
C 70	51	32.1	1434	1	US-09-023-655-481	Sequence 481, App
C 71	51	32.1	1845	1	US-07-732-962A-1	Sequence 1, Appli
C 72	51	32.1	1845	2	PCT-US92-06106-1	Sequence 1, Appli
C 73	51	32.1	2256	2	US-08-318-826A-5	Sequence 5, Appli
C 74	51	32.1	2256	2	US-08-370-156-1	Sequence 1, Appli
C 75	51	32.1	2256	3	US-08-814-095-1	Sequence 1, Appli
C 76	51	32.1	3016	2	US-08-318-826A-7	Sequence 7, Appli
C 77	51	32.1	3016	2	US-08-370-156-5	Sequence 5, Appli
C 78	51	32.1	3016	3	US-08-814-095-5	Sequence 5, Appli
C 79	51	32.1	3096	2	US-08-318-826A-6	Sequence 6, Appli
C 80	51	32.1	3096	2	US-08-370-156-3	Sequence 3, Appli
C 81	51	32.1	3096	3	US-08-814-095-3	Sequence 3, Appli
C 82	51	32.1	3911	4	US-09-566-921-61	Sequence 61, Appli
C 83	51	32.1	7672	4	US-09-220-132-24	Sequence 24, Appli
C 84	51	32.1	8310	3	US-08-870-126-11	Sequence 11, Appli
C 85	51	32.1	8310	4	US-09-445-247-11	Sequence 11, Appli

Db 1976 GCACCGCGCTGCGCCAGCCAGCACA 2005

RESULT 3

US-09-344-195-3
; Sequence 3, Application US/09344195
; Patent No. 6210662
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; Ruegg, Curtis L.
; Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSP-HER-2 fusion gene; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-344-195-3

Alignment Scores:
Pred. No.: 0.00569 Length: 2385
Score: 84.00 Matches: 21
Percent Similarity: 70.00% Conservative: 0
Best Local Similarity: 70.00% Mismatches: 5
Query Match: 52.83% Indels: 4
DB: 3 Gaps: 2

SEQ3-SEQ5 (1-30) x US-09-344-195-3 (1-2385)

Qy 1 AsplyGlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAenGluAspLeu 20

Db 1925 GACAAGGCGCTGCCCGCCGAGCAGAGCCCTCTGAGTCCCTCGAG----- 1975

Qy 21 GlyProAla---SerProLeuAspSerThr 29

Db 1976 GCACCGCGCTGCGCCAGCCAGCACA 2005

RESULT 4

US-08-776-251-3
; Sequence 3, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,251
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-776-251-3

Alignment Scores:
Pred. No.: 0.000697 Length: 153
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 3 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-776-251-3 (1-153)

Qy 1 AsplyGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15

Db 10 GACAAGGCGCTGCCCGCCGAGCAGAGCCCTCTGAGCTCC 54

RESULT 5

US-09-200-355-3
; Sequence 3, Application US/09200355
; Patent No. 6451524
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/09/200,355
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 201
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-200-355-3

Alignment Scores:
Pred. No.: 0.000983 Length: 201
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-200-355-3 (1-201)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
DB 116 GACAGAGGGCGCCCGCCGAGCAGAGAGCCCGCCUUCAGCUCC 160

RESULT 6
US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION NUMBER: US/08/776,251
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-776-251-10

Alignment Scores:
Pred. No.: 0.00576 Length: 816
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 3 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-776-251-10 (1-816)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
DB 93 GACAGAGGGCGCCCGCCGAGCAGAGCCCGCCCTGTGACGTCC 137

RESULT 7
US-08-625-101-1
; Sequence 1, Application US/08625101

Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disig, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3765
US-08-625-101-1

Alignment Scores:
Pred. No.: 0.0397 Length: 3768
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 2 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-625-101-1 (1-3768)

QY 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
|||||
DB 1915 GACAGAGGGTGTGCCCCCGCAGCAGAGCCGCTCTGACGTCC 1959

RESULT 8
US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston

APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
CORRESPONDENCE ADDRESS:
ADDRESS: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-229-515A-9

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-229-515A-9 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2089 GACAAGGGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTC 2133

RESULT 12
US-09-663-834A-3
Sequence 3, Application US/09663834A
Patent No. 6613567
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
FILE REFERENCE: RTS-0033
CURRENT APPLICATION NUMBER: US/09/663,834A
CURRENT FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 48
SEQ ID NO 3
LENGTH: 4473
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (175)...(3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0.0494 Length: 4473
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-663-834A-3 (1-4473)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2089 GACAAGGGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTC 2133

RESULT 13
US-08-229-515A-9
Sequence 9, Application US/08229515A
Patent No. 5518885
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN

TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,515A
FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-229-515A-9

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-229-515A-9 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAGGGCTGCCCCCGAGCAGAGAGCCGCTCTGACGTC 2109

RESULT 14
US-08-645-865-9
Sequence 9, Application US/08645865
Patent No. 5654406
GENERAL INFORMATION:
APPLICANT: RAZIUDIN
APPLICANT: SARKAR, FAZLUL H
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
TITLE OF INVENTION: NEOPLASTIC DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: NEEDLE & ROSENBERG PC
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
COUNTRY: usa
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,865
FILING DATE: 14 MAY 1996
CLASSIFICATION: 435

```

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-167-322-4 (1-4530)

Qy 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
| | | | |
Db 2065 GACAAAGGGCTGCCCCCGGACGACGAGGACGAGCCCTCTGACGTCC 2109

RESULT 16
US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-527-487-1 (1-4530)

Qy 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
| | | | |
Db 2065 GACAAAGGGCTGCCCCCGGACGACGAGGACGAGCCCTCTGACGTCC 2109

RESULT 17
US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Express
; TITLE OF INVENTION: and Correlation of Levels Thereof With S
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 0.0501 Length: 4530
Score: 80.00 Matches: 15

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-877-177A-11 (1-4530)

QY 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 2065 GACAAGGGTGTCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2109

RESULT 18
US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GEMT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 0.124 Length: 9274
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-811-115-1 (1-9274)

QY 1 AspLysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
DB 3645 GACAAGGGTGTCCCGCCGAGCAGAGAGCCCTCTGACGTCC 3689

RESULT 19
US-08-229-515A-14
; Sequence 14, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIYUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30103
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-14
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FILING DATE: 19 APR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERRYMAN, DAVID G
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414.608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-229-515A-14

Alignment Scores:
Pred. No.: 0.328 Length: 3955
Score: 74.00 Matches: 13
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 86.67% Mismatches: 0
Query Match: 46.54% Indels: 0
DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-229-515A-14 (1-3955)

QY 16 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
DB 2999 CAGAACGAGGACTTGGGCCCATCCAGCCCATGGACAGTACCTTC 3043

RESULT 20
US-08-645-865-14
; Sequence 14, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIYUDDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-14

Alignment Scores:
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```

Pred. No.: 0.328 Length: 3955
Score: 74.00 Matches: 13
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 86.67% Mismatches: 0
Query Match: 46.54% Indels: 0
DB: 1 Gaps: 0

SEQ3-SEQ5 (1-30) x US-08-645-865-14 (1-3955)

Qy 16 GlnAsnGluAspLeuGlyProAlaSerProLeuAspSerThrPhe 30
Db 2999 CAGACGAGGACTTGGGCCCATCCAGGCCCATGACAGTACCTTC 3043

RESULT 21
US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754, 250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(111282)
; OTHER INFORMATION: n = A, T, C or G
US-09-754-250-3

Alignment Scores:
Pred. No.: 3.71e+03 Length: 111282
Score: 59.00 Matches: 11
Percent Similarity: 56.52% Conservative: 2
Best Local Similarity: 47.83% Mismatches: 10
Query Match: 37.11% Indels: 0
DB: 4 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-754-250-3 (1-111282)

Qy 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
Db 15912 GGCTGTCCAGCCCTGCTCATGCTCCCTCCACTATGGCGAGGAGCTCATCCCTGCTCTCCC 15853

Qy 23 AlaserPro 25
Db 15852 ACCGAGCCC 15844

RESULT 22
US-08-451-947-1/c
; Sequence 1, Application US/08451947
; Patent No. 5702906
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

Pred. No.: 6.47 Length: 634
Score: 58.50 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 36.79% Indels: 1
DB: 1 Gaps: 1

SEQ3-SRQ5 (1-30) x US-08-451-947-1 (1-634)

Qy 3 GlyCysProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
Db 221 GGGGCACCTGCTGACTCCCGAAGGCCCTCCAGCAGGAGCAGAGGGGGGCCCA 162

Qy 23 Ala---SerProLeuAspSerThr 29
Db 161 GCAGGGGCACCCCTAGACAGGACT 138

RESULT 23
US-08-424-826A-1/c
; Sequence 1, Application US/08424826A
; Patent No. 5830858
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Arnon
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
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; FILING DATE: 26-MAY-1995
; PRIOR APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0666P2C1D2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 634 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-928-694-1

Alignment Scores:
Pred. No.: 6.47 Length: 634
Score: 58.50 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 9
Query Match: 36.79% Indels: 1
DB: Gaps: 1

SEQ3-SQ05 (1-30) x US-08-928-694-1 (1-634)
Qy 3 GlyCyProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro 22
Db 221 GGCGGCACCTGCTGACTCCCGAAGGCCCGCCAGCTCCAGCAGGAAGAGAGGGGGCCCCA 162
Qy 23 Ala---SerProLeuAspSerThr 29
Db 161 GCAGGGGCACCCTTAGACAGGACT 138

RESULT 25
US-08-450-842-1/c
; Sequence 1, Application US/08450842
; Patent No. 6506728
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/426419

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FILING DATE:	19-APR-1995				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	08/030013				
FILING DATE:	22-MAR-1993				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	07/648482				
FILING DATE:	31-JAN				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	07/587707				
FILING DATE:	1991				
ATTORNEY/AGENT INFORMATION:					
NAME:	Torchia, Timothy E.				
REGISTRATION NUMBER:	36,700				
REFERENCE/DOCKET NUMBER:	666P2C1D3				
TELECOMMUNICATION INFORMATION:					
TELEPHONE:	415/225-8674				
TELEFAX:	415/952-9881				
TELEX:	910/371-7168				
INFORMATION FOR SEQ ID NO:	1:				
SEQUENCE CHARACTERISTICS:					
LENGTH:	634 bases				
TYPE:	nucleic acid				
STRANDEDNESS:	single				
TOPOLOGY:	linear				
US-08-450-842-1					
Alignment Scores:					
Pred. No.:	6.47	Length:	634		
Score:	58.50	Matches:	13		
Percent Similarity:	64.29%	Conservative:	5		
Best Local Similarity:	46.43%	Mismatches:	9		
Query Match:	36.79%	Indels:	1		
DB:	4	Gaps:	1		
SEQ3-SEQ5 (1-30) x US-08-450-842-1 (1-634)					
Qy	3 GlyCyProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro	22			
Db	221 GGGGCACCTGCTCACTCCCGAAGGCCCTCCAGCAGGAGCAGAGGGGGCCCCA	162			
Qy	23 Ala---SerProLeuAspSerThr	29			
Db	161 GCAGGGGCACCCCTAGACAGGACT	138			
RESULT 26					
US-08-451-390-1/c					
Sequence 1, Application US/08451390					
GENERAL INFORMATION:					
APPLICANT: GENENTECH, INC.					
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR					
NUMBER OF SEQUENCES: 100					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Genentech, Inc.					
STREET: 460 Point San Bruno Blvd					
CITY: South San Francisco					
STATE: California					
COUNTRY: USA					
ZIP: 94080					
COMPUTER READABLE FORM:					
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk					
OPERATING SYSTEM: PC-DOS/MS-DOS					
SOFTWARE: patin (Genentech)					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/08/451,390					
FILING DATE:					
CLASSIFICATION: 536					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: 08/426419					
FILING DATE: 19-APR-1995					
PRIOR APPLICATION DATA:					
REGISTRATION NUMBER: 27,043					

FILING DATE:	19-APR-1995				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	08/030013				
FILING DATE:	22-MAR-1993				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	07/648482				
FILING DATE:	31-JAN				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	07/587707				
FILING DATE:	1991				
ATTORNEY/AGENT INFORMATION:					
NAME:	Torchia, Timothy E.				
REGISTRATION NUMBER:	36,700				
REFERENCE/DOCKET NUMBER:	666P2C1D3				
TELECOMMUNICATION INFORMATION:					
TELEPHONE:	415/225-8674				
TELEFAX:	415/952-9881				
TELEX:	910/371-7168				
INFORMATION FOR SEQ ID NO:	1:				
SEQUENCE CHARACTERISTICS:					
LENGTH:	634 bases				
TYPE:	nucleic acid				
STRANDEDNESS:	single				
TOPOLOGY:	linear				
US-08-450-842-1					
Alignment Scores:					
Pred. No.:	6.47	Length:	634		
Score:	58.50	Matches:	13		
Percent Similarity:	64.29%	Conservative:	5		
Best Local Similarity:	46.43%	Mismatches:	9		
Query Match:	36.79%	Indels:	1		
DB:	4	Gaps:	1		
SEQ3-SEQ5 (1-30) x US-08-450-842-1 (1-634)					
Qy	3 GlyCyProAlaGluGlnArgAlaSerProLeuThrSerGlnAsnGluAspLeuGlyPro	22			
Db	221 GGGGCACCTGCTCACTCCCGAAGGCCCTCCAGCAGGAGCAGAGGGGGCCCCA	162			
Qy	23 Ala---SerProLeuAspSerThr	29			
Db	161 GCAGGGGCACCCCTAGACAGGACT	138			
RESULT 26					
US-08-451-390-1/c					
Sequence 1, Application US/08451390					
GENERAL INFORMATION:					
APPLICANT: GENENTECH, INC.					
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR					
NUMBER OF SEQUENCES: 100					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Genentech, Inc.					
STREET: 460 Point San Bruno Blvd					
CITY: South San Francisco					
STATE: California					
COUNTRY: USA					
ZIP: 94080					
COMPUTER READABLE FORM:					
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk					
OPERATING SYSTEM: PC-DOS/MS-DOS					
SOFTWARE: patin (Genentech)					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/08/451,390					
FILING DATE:					
CLASSIFICATION: 536					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: 08/426419					
FILING DATE: 19-APR-1995					
PRIOR APPLICATION DATA:					
REGISTRATION NUMBER: 27,043					

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2004, 06:43:09 ; Search time 267 Seconds
(without alignments)
512.584 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -NMAR=HOLLERAN480 @CGN 1 1 879 @runat 07062004 152436_24797
-NCPU=6 -ICPU=3 -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.2*
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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

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2	80	50.3	884	16	US-10-412-804A-7	Sequence 7, Appli
3	80	50.3	1479	16	US-10-412-804A-1	Sequence 1, Appli
4	80	50.3	2164	16	US-10-412-804A-5	Sequence 5, Appli
5	80	50.3	3765	15	US-10-207-498-5	Sequence 5, Appli
6	80	50.3	3768	9	US-09-811-123-8	Sequence 8, Appli
7	80	50.3	3768	9	US-09-811-115-2	Sequence 2, Appli
8	80	50.3	3768	9	US-09-854-356-9	Sequence 9, Appli
9	80	50.3	3768	9	US-09-930-125-1	Sequence 1, Appli
10	80	50.3	3768	13	US-09-984-092-3	Sequence 3, Appli
11	80	50.3	3768	13	US-10-280-576-3	Sequence 3, Appli
12	80	50.3	3768	13	US-09-765-973-1	Sequence 1, Appli
13	80	50.3	3768	15	US-10-313-644-1	Sequence 1, Appli
14	80	50.3	4473	10	US-09-441-411-5	Sequence 5, Appli
15	80	50.3	4473	15	US-10-146-473-32	Sequence 32, Appli
16	80	50.3	4473	15	US-10-207-655-44	Sequence 44, Appli
17	80	50.3	4473	15	US-10-101-510-81	Sequence 81, Appli
18	80	50.3	4530	9	US-09-877-177-11	Sequence 11, Appli
19	80	50.3	4530	13	US-10-392-113-45	Sequence 45, Appli
20	80	50.3	4530	13	US-10-426-836-11	Sequence 11, Appli
21	80	50.3	4530	15	US-10-177-293-125	Sequence 125, Appli
22	80	50.3	4530	15	US-10-007-926A-119	Sequence 119, Appli
23	80	50.3	4530	15	US-10-338-730-1	Sequence 1, Appli
24	80	50.3	4530	15	US-10-101-510-124	Sequence 124, Appli
25	80	50.3	4530	16	US-10-116-275-131	Sequence 131, Appli
26	80	50.3	4530	16	US-10-272-437A-27	Sequence 27, Appli
27	80	50.3	4530	16	US-10-117-937-595	Sequence 595, Appli
28	80	50.3	4530	16	US-10-159-563-208	Sequence 208, Appli
29	80	50.3	4530	16	US-10-435-696-10	Sequence 10, Appli
30	80	50.3	4543	9	US-09-769-508-1	Sequence 1, Appli
31	80	50.3	4606	10	US-09-971-392-70	Sequence 70, Appli
32	80	50.3	4642	15	US-10-198-846-10896	Sequence 10896, A
33	80	50.3	9274	9	US-09-811-123-7	Sequence 7, Appli
34	80	50.3	9274	9	US-09-811-115-1	Sequence 1, Appli
35	79	49.7	1115	13	US-09-925-298-165	Sequence 165, Appli
36	79	49.7	1115	15	US-10-102-806-165	Sequence 165, Appli
37	79	49.7	1713	15	US-10-378-393-14	Sequence 14, Appli
38	79	49.7	1755	9	US-09-930-125-6	Sequence 6, Appli
39	79	49.7	1767	9	US-09-930-125-4	Sequence 4, Appli
40	79	49.7	1773	9	US-09-930-125-7	Sequence 7, Appli
41	79	49.7	1806	9	US-09-930-125-5	Sequence 5, Appli
42	79	49.7	2411	15	US-10-378-393-10	Sequence 10, Appli
43	74	46.5	2149	16	US-10-412-804A-9	Sequence 9, Appli
44	74	46.5	3771	9	US-09-854-356-11	Sequence 11, Appli
45	74	46.5	3955	9	US-09-870-759-117	Sequence 117, Appli
46	74	46.5	3955	9	US-09-854-356-10	Sequence 10, Appli
47	74	46.5	3955	10	US-09-751-708A-117	Sequence 117, Appli
48	62	39.0	2159	16	US-10-094-749-98	Sequence 98, Appli
49	62	39.0	3837	16	US-10-367-978-10	Sequence 10, Appli
50	62	39.0	4591	13	US-10-342-887-29	Sequence 29, Appli
51	62	39.0	4591	13	US-10-172-118-29	Sequence 29, Appli
52	62	39.0	14427	15	US-10-156-761-1540	Sequence 1540, Ap
53	62	39.0	23432	9	US-09-764-869-1332	Sequence 1332, Ap
54	62	39.0	23432	15	US-10-091-504-1332	Sequence 1332, Ap
55	62	39.0	23432	16	US-10-227-577-1332	Sequence 1332, Ap
56	62	39.0	100301	17	US-10-450-826-83	Sequence 83, Appli
57	62	39.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
58	61	38.4	22801	12	US-10-052-482-40	Sequence 40, Appli
59	59	37.1	11252	13	US-10-425-114-1764	Sequence 1764, Ap
60	59	37.1	111282	14	US-10-094-989-3	Sequence 3, Appli
61	58.5	36.8	633	10	US-09-788-188-12	Sequence 12, Appli
62	58.5	36.8	634	8	US-08-450-842-1	Sequence 1, Appli
63	58.5	36.8	634	13	US-10-371-003-1	Sequence 1, Appli
64	58.5	36.8	1404	15	US-10-155-785-13	Sequence 13, Appli
65	57.5	36.2	363	10	US-09-318-995-28706	Sequence 28706, A
66	57	35.8	297	9	US-09-783-590-11498	Sequence 11498, A
67	57	35.8	761	17	US-10-304-116-11	Sequence 11, Appli
68	57	35.8	1938	15	US-10-422-264-25	Sequence 25, Appli
69	57	35.8	2316	15	US-10-422-264-27	Sequence 27, Appli
70	57	35.8	2604	15	US-10-422-264-23	Sequence 23, Appli
71	57	35.8	3320	9	US-09-862-658-1	Sequence 1, Appli
72	57	35.8	3320	15	US-10-175-696-22	Sequence 22, Appli

Publication No. US2003010888A1
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew
 APPLICANT: Gout, Ivan
 APPLICANT: Stockert, Elisabeth
 APPLICANT: Gure, Ali
 APPLICANT: Chen, Yao-Tsang
 APPLICANT: Old, Lloyd
 TITLE OF INVENTION: Breast Cancer Antigens
 FILE REFERENCE: L00461/70130(JRV)
 CURRENT APPLICATION NUMBER: US/10/146,473
 CURRENT FILING DATE: 2002-05-15
 PRIOR APPLICATION NUMBER: US 60/291,150
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 82
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 32
 LENGTH: 4473
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-146-473-32

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-146-473-32 (1-4473)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2089 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2133

RESULT 16

US-10-207-655-44
 Sequence 44, Application US/10207655
 Publication No. US20030118592A1
 GENERAL INFORMATION:
 APPLICANT: Ledbetter, Jeffrey A.
 APPLICANT: Hayden-Ledbetter, Martha S.
 TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 FILE REFERENCE: 390069.401C1
 CURRENT APPLICATION NUMBER: US/10/207,655
 CURRENT FILING DATE: 2002-07-25
 NUMBER OF SEQ ID NOS: 426
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 44
 LENGTH: 4473
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-207-655-44

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-207-655-44 (1-4473)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2089 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2133

RESULT 17

US-10-101-510-81
 Sequence 81, Application US/10101510
 Publication No. US20030148295A1

GENERAL INFORMATION:
 APPLICANT: WAN, JACKSON
 APPLICANT: WANG, YIXIN
 TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
 FILE REFERENCE: 15117.0012
 CURRENT APPLICATION NUMBER: US/10/101,510
 CURRENT FILING DATE: 2002-03-20
 PRIOR APPLICATION NUMBER: 60/276,947
 PRIOR FILING DATE: 2001-03-20
 NUMBER OF SEQ ID NOS: 805
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 81
 LENGTH: 4473
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-101-510-81

Alignment Scores:
 Pred. No.: 0.0279 Length: 4473
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-101-510-81 (1-4473)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2089 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2133

RESULT 18

US-09-877-177-11
 Sequence 11, Application US/09877177
 Publication No. US20020192652A1
 GENERAL INFORMATION:
 APPLICANT: Peter V. Danenberg et al.
 TITLE OF INVENTION: Method of determining Epidermal Growth
 Factor Receptor and HER2-New Gene Expression
 FILE REFERENCE: 11220/120
 CURRENT APPLICATION NUMBER: US/09/877,177
 CURRENT FILING DATE: 2001-06-11
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 4530
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-877-177-11

Alignment Scores:
 Pred. No.: 0.0283 Length: 4530
 Score: 80.00 Matches: 15
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.31% Indels: 0
 DB: 9 Gaps: 0

SEQ3-SEQ5 (1-30) x US-09-877-177-11 (1-4530)

QY 1 AsPLySGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
 |||||
 DB 2065 GACAGGGCTGCCCGCCGAGCAGAGAGCCCTCTGACGTCC 2109

RESULT 19

US-10-392-113-45
 Sequence 45, Application US/10392113
 Publication No. US20030224993A1
 GENERAL INFORMATION:
 APPLICANT: Land, Hartmut
 APPLICANT: Deleu, Laurent
 TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
 OF CANCER CELLS

```

; FILE REFERENCE: 21108_0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-392-113-45 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTC 2109

RESULT 20
US-10-426-836-11
; Sequence 11, Application US/10426836
; Publication No. US20030211530A1
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/169
; CURRENT APPLICATION NUMBER: US/10/426,836
; CURRENT FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-836-11

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 13 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-426-836-11 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTC 2109

RESULT 21
US-10-177-293-125
; Sequence 125, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:

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```

; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzstai, Lajos
; APPLICANT: Mexic, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-125

Alignment Scores:
Pred. No.: 0.0283 Length: 4530
Score: 80.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.31% Indels: 0
DB: 15 Gaps: 0

SEQ3-SEQ5 (1-30) x US-10-177-293-125 (1-4530)

Qy 1 AsplysGlyCysProAlaGluGlnArgAlaSerProLeuThrSer 15
Db 2065 GACAAGGGCTGCCCGCCGAGCAGAGCCAGCCCTCTGACGTC 2109

RESULT 22
US-10-007-926A-119
; Sequence 119, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07

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Search completed: June 8, 2004, 09:24:28
Job time : 282 secs